

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2004, 13:34:19 ; Search time 195.614 Seconds
(without alignment)

278.934 Million cell updates/sec

Title: US-08-836-455-4

Sequence score: 816
1 MECSWFLFLSLTTGVHSGQ.....TVSSAKTPPPVPLVPGSL 153

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA.*

1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubppaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*
20: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	816	100.0	153	9	US-09-861-294-4
2	816	100.0	153	14	US-10-367-506-4
3	574.5	70.4	468	10	US-09-795-515-7
4	574.5	70.4	468	15	US-10-704-352-7
5	574.5	70.4	468	15	US-10-704-071-7
6	574.5	70.4	468	16	US-10-682-845-38
7	574.5	70.4	468	17	US-10-703-963-7
8	565	69.2	467	17	US-10-742-405-12
9	560.5	68.7	464	14	US-10-216-484-9
10	560.5	68.7	464	14	US-10-384-933-9
11	554.5	68.0	468	9	US-09-903-327A-6
12	554.5	68.0	468	9	US-09-903-327A-2
13	554.5	68.0	493	9	US-09-903-327A-13

14	554.5	68.0	510	9	US-09-903-327A-12	Sequence 12, Appl
15	554.5	68.0	597	9	US-09-903-327A-11	Sequence 11, Appl
16	554.5	68.0	613	9	US-09-903-327A-14	Sequence 14, Appl
17	552.5	67.7	136	14	US-10-160-232-88	Sequence 88, Appl
18	543	66.5	238	14	US-10-336-210-3	Sequence 3, Appl
19	543	66.5	272	14	US-10-336-210-7	Sequence 7, Appl
20	540	66.2	135	14	US-10-244-821-91	Sequence 91, Appl
21	539.5	66.1	180	9	US-09-748-960-6	Sequence 6, Appl
22	536	65.7	152	16	US-10-642-120-2	Sequence 2, Appl
23	536	65.7	152	16	US-10-642-060-2	Sequence 2, Appl
24	536	65.7	152	16	US-10-642-122-2	Sequence 2, Appl
25	536	65.7	152	16	US-10-642-124-2	Sequence 2, Appl
26	536	65.7	152	16	US-10-621-269-2	Sequence 2, Appl
27	536	65.7	152	16	US-10-620-850-2	Sequence 2, Appl
28	536	65.7	152	17	US-10-642-118-2	Sequence 2, Appl
29	536	65.7	152	17	US-10-642-117-2	Sequence 2, Appl
30	536	65.7	152	17	US-10-642-119-2	Sequence 2, Appl
31	536	65.7	152	17	US-10-642-099-2	Sequence 2, Appl
32	536	65.7	237	14	US-10-336-210-2	Sequence 2, Appl
33	536	65.7	271	14	US-10-336-210-6	Sequence 6, Appl
34	530	65.0	139	10	US-09-269-921-105	Sequence 105, App
35	530	65.0	139	10	US-09-509-098-4	Sequence 4, Appl
36	530	65.0	139	14	US-10-218-253-105	Sequence 105, App
37	528	64.7	139	10	US-09-269-921-126	Sequence 126, App
38	528	64.7	139	10	US-09-509-098-98	Sequence 98, Appl
39	528	64.7	139	13	US-10-006-773-13	Sequence 13, Appl
40	528	64.7	139	14	US-10-218-253-126	Sequence 126, App
41	522.5	64.0	140	14	US-10-096-928-6	Sequence 6, Appl
42	522.5	64.0	140	14	US-10-096-964-6	Sequence 6, Appl
43	522.5	64.0	164	17	US-10-471-475A-23	Sequence 23, Appl
44	522	64.0	135	14	US-10-389-156-60	Sequence 60, Appl
45	522	64.0	135	15	US-10-389-417-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-09-861-294-4 ; Sequence 4, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; CURRENT FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(19)
US-09-861-294-4

Query Match 100.0%; Score 816; DB 9; Length 153;
Best Local Similarity 100.0%; Pred. No. 7.8e-61;

Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MECSWFLFLSLTTGVHSGQAYIQSGAELVRSAGSVKRSCKRAGYTLTSSNMHWKQTP 60
DB 1 MECSWFLFLSLTTGVHSGQAYIQSGAELVRSAGSVKRSCKRAGYTLTSSNMHWKQTP 60
QY 61 GQGLEWIGNIPFONGTYYNOKFKKASLTADTSSSTATMQLSSLTSEDSAVYFCARGNW 120

Db 61 GGGLEWIGNIFPGNGDITVYNOKEFGKASLTADTSSSTAYMOISLTSEDSAVYFCARGNW 120
Qy 121 EGALDYWGQGTSTVTSASAKTTPPPVYPLVPGSL 153
Db 121 EGALDYWGQGTSTVTSASAKTTPPPVYPLVPGSL 153

RESULT 2

US-10-367-506-4
Sequence 4, Application US/10367506
Publication No. US20030152575A1
GENERAL INFORMATION:
APPLICANT: Malaya CHATTERJEE
APPLICANT: Kenneth A. POON
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
FILE REFERENCE: TOWERS BEARING HMF6 AND CEA ANTIGENS
CURRENT APPLICATION NUMBER: US/10/367,506
PRIOR FILING DATE: 2003-02-13
PRIOR APPLICATION NUMBER: US/09/861,294
PRIOR FILING DATE: 2001-05-17
PRIOR APPLICATION NUMBER: 60/049,540
PRIOR FILING DATE: 1997-06-13
PRIOR APPLICATION NUMBER: 09/096,244
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 4
LENGTH: 153
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: SIGNAL
LOCATION: (1)...(19)
US-10-367-506-4

Query Match 100.0%; Score 816; DB 14; Length 153;
Best Local Similarity 100.0%; Pred. No. 7,8e-61;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MECSWVFLFLISITTTGVHQAAYLQOSGAEIVRSGASVSKSCASGYTLTSYNNHWKQTP 60
Db 1 MECSWVFLFLISITTTGVHQAAYLQOSGAEIVRSGASVSKSCASGYTLTSYNNHWKQTP 60
Qy 61 GGGLEWIGNIFPGNGDITVYNOKEFGKASLTADTSSSTAYMOISLTSEDSAVYFCARGNW 120
Db 61 GGGLEWIGNIFPGNGDITVYNOKEFGKASLTADTSSSTAYMOISLTSEDSAVYFCARGNW 120
Qy 121 EGALDYWGQGTSTVTSASAKTTPPPVYPLVPGSL 153
Db 121 EGALDYWGQGTSTVTSASAKTTPPPVYPLVPGSL 153

RESULT 3

US-09-795-515-7
Sequence 7, Application US/09795515
Publication No. US20030039645A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1r18
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatto
REGISTRATION NUMBER: 35,719
TELEPHONE/DOCKET NUMBER: CARP-0057
TELEPHONE: (215) 568-3100
FAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Protein
US-09-795-515-7

Query Match 70.4%; Score 574.5; DB 10; Length 468;
Best Local Similarity 74.8%; Pred. No. 5e-40;
Matches 113; Conservative 8; Mismatches 29; Indels 1; Gaps 1;

Qy 1 MECSWVFLFLISITTTGVHQAAYLQOSGAEIVRSGASVSKSCASGYTLTSYNNHWKQTP 60
Db 1 MERHWIFLLISVYAGVHQAAYLQOSGAEIVRSGASVSKSCASGYTLTSYNNHWKQTP 60
Qy 61 GGGLEWIGNIFPGNGDITVYNOKEFGKASLTADTSSSTAYMOISLTSEDSAVYFCARGNW 119
Db 61 GGGLEWIGNIFPGNGDITVYNOKEFGKASLTADTSSSTAYMOISLTSEDSAVYFCARGNW 120
Qy 120 EGALDYWGQGTSTVTSASAKTTPPPVYPLV 150
Db 121 DHYCLDYWGQGTTLTVSSAKTTAPSVYPLAP 151

RESULT 4

US-10-704-352-7
Sequence 7, Application US/10704352
Publication No. US20040071693A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Athwal, Diljeet S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/704,352
FILING DATE: 07-Nov-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/795,515
FILING DATE: 28-FEB-2001
APPLICATION NUMBER: 08/846,658
FILING DATE: 01-MAY-1997

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2004, 13:29:00 ; Search time 16.4295 Seconds
(without alignments)
617.586 Million cell updates/sec

Title: US-08-836-455-4

Perfect score: 816
Sequence: 1 MEC5WVFLFLSLTTGVHSQ.....TVSSAKTTPPVPLVPGSL 153

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/aa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/aa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/aa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/aa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/aa/PCUS_COMB.pep.*
6: /cgn2_6/prodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	816	100.0	153	3	US-09-096-244-4
2	574.5	70.4	468	2	US-08-303-569B-7
3	574.5	70.4	468	2	US-08-116-247-7
4	574.5	70.4	468	4	US-09-795-515-7
5	574.5	70.4	468	4	US-09-348-224-7
6	568.5	69.7	151	3	US-08-513-968-34
7	568	69.6	561	3	US-09-192-545-2
8	565	69.2	140	4	US-09-124-138-44
9	554.5	68.0	464	1	US-08-353-600-36
10	541.5	66.4	138	4	US-09-254-180C-143
11	535	65.6	235	3	US-08-444-644-19
12	535	65.6	235	3	US-08-332-246A-19
13	534	65.4	139	1	US-08-253-877C-8
14	534	65.4	139	2	US-08-452-164A-8
15	533	65.3	138	3	US-08-603-024-2
16	532	65.2	235	3	US-08-444-644-28
17	532	65.2	235	3	US-08-444-644-42
18	532	65.2	235	3	US-08-332-246A-28
19	532	65.2	235	3	US-08-332-246A-42
20	531.5	65.1	136	5	PCT-US93-11611-4
21	530	65.0	139	4	US-09-269-921-105
22	528	64.7	139	4	US-09-269-921-126
23	525.5	64.4	140	3	US-08-579-378A-4
24	525.5	64.4	140	5	PCT-US93-11612-4
25	522.5	64.0	140	1	US-08-476-875-6
26	522.5	64.0	140	4	US-08-475-813-6
27	522	64.0	135	1	US-07-634-278-69

28	522	64.0	135	1	US-08-477-728-69	Sequence 69, Appl
29	522	64.0	135	1	US-08-474-040-69	Sequence 69, Appl
30	522	64.0	135	1	US-08-487-200-69	Sequence 69, Appl
31	522	64.0	135	3	US-08-484-537-69	Sequence 69, Appl
32	520.5	63.8	140	3	US-08-475-815B-11	Sequence 11, Appl
33	520.5	63.8	219	4	US-09-254-180C-131	Sequence 131, Appl
34	520.5	63.8	219	4	US-09-254-180C-181	Sequence 181, Appl
35	518	63.5	233	3	US-08-444-644-33	Sequence 33, Appl
36	518	63.5	233	3	US-08-232-246A-33	Sequence 33, Appl
37	516.5	63.3	150	2	US-08-400-115-2	Sequence 153, Appl
38	512	62.7	137	4	US-09-647-468-153	Sequence 153, Appl
39	512	62.7	137	4	US-09-647-468-154	Sequence 154, Appl
40	511.5	62.7	219	4	US-09-254-180C-180	Sequence 180, Appl
41	511.5	62.7	445	1	US-08-353-400-33	Sequence 33, Appl
42	511	62.6	139	1	US-08-137-117D-35	Sequence 35, Appl
43	511	62.6	139	2	US-08-436-717-35	Sequence 35, Appl
44	511	62.6	139	2	US-08-656-586-4	Sequence 4, Appl
45	510	62.5	137	1	US-08-392-419-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-096-244-4
Sequence 4, Application US/09096244
Patent No. 6274143
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,244
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Polizzi, Catherine M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 30414-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 153 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-096-244-4

Query Match 100.0%; Score 816; DB 3; Length 153;
Best local similarity 100.0%; Pred. No. 9.8e-61;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MEC5WVFLFLSLTTGVHSQAVLQSGAEVLSGASVSKSCASGYTLTSYNNHWVKQP 60
DB 1 MEC5WVFLFLSLTTGVHSQAVLQSGAEVLSGASVSKSCASGYTLTSYNNHWVKQP 60

QY 61 GGGLEWIMGNFPENGNGTYNNOKERKASLTADTSSSTAYWMOISSLTSEDSAYVFCARGNN 120

Dd 61 GGGLEWIMGNFPENGNGTYNNOKERKASLTADTSSSTAYWMOISSLTSEDSAYVFCARGNN 120

QY 121 EGALDYMGGSTSYTUSAAKTPPPRYPLVPGSL 153

Dd 121 EGALDYMGGSTSYTUSAAKTPPPRYPLVPGSL 153

```

1  RESULT 2
2  US-08-303-569B-7
3  ; Sequence 7, Application US/08303569B
4  ; Patent No. 5859205
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Adair, John R.
7  ; APPLICANT: Athwal, Diljeet S.
8  ; APPLICANT: Emtage, John S.
9  ; TITLE OF INVENTION: Humanised Antibodies
10 ; NUMBER OF SEQUENCES: 31
11 ; CORRESPONDENCE ADDRESS:
12 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205Stris
13 ; STREET: One Liberty Place - 46th Floor
14 ; CITY: Philadelphia
15 ; STATE: PA
16 ; COUNTRY: USA
17 ; ZIP: 19103
18 ; COMPUTER READABLE FORM:
19 ; MEDIUM TYPE: Floppy disk
20 ; COMPUTER: IBM PC compatible
21 ; OPERATING SYSTEM: PC-DOS/MS-DOS
22 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
23 ; CURRENT APPLICATION DATA:
24 ; APPLICATION NUMBER: US/08/303,569B
25 ; FILING DATE: 07-SEP-1994
26 ; CLASSIFICATION:
27 ; ATTORNEY/AGENT INFORMATION:
28 ; NAME: Trujillo, Doreen Yacht
29 ; REGISTRATION NUMBER: 35,719
30 ; REFERENCE/DOCKET NUMBER: CARP-0032
31 ; TELECOMMUNICATION INFORMATION:
32 ; TELEPHONE: (215) 568-3100
33 ; TELEFAX: (215) 568-3439
34 ; INFORMATION FOR SEQ ID NO: 7:
35 ; SEQUENCE CHARACTERISTICS:
36 ; LENGTH: 468 amino acids
37 ; TYPE: amino acid
38 ; TOPOLOGY: linear
39 ; MOLECULE TYPE: protein
40 ; US-08-303-569B-7

```

	70.4%;	Score 574.5;	DB 2;	Length 468;
Query March	Best Local Similarity 74.8%;	Pred. No. 4e-40;	Mismatches 113;	Conservative 8; Mismatches 29; Indels 1; Gaps 1
OY	1 MECSWFELPLSLITTVGSHQAYLLOOSGAEVLRSGSATVMSCKSGTTLTSYNMHWKQTPE			60
Db	1 MERHMFLLLSLTAVTGVSHQVQLQSSGHELARPAASATVMSCKSGGTFRYYTMHWKRP			60
OY	61 GOELEWIGNIIFPONGDITYNOKFEKGKSLADITSSSTAYNQIISLTSEDSAAVFCAR-GN			119
Db	61 GOELEWTGINSRGYTYNNOKFKDKAKILLTDKSSSTAYNQJLSSLESDSAIYYCAKYDD			120
OY	120 WEGALDYMGQGSVTYSVASAKTTTPPYLVPIVP			150
Db	121 DHYCUDYMGQGITTLTVSSAKTTAPSVPLAP			151

RESULT 3
US-08-116-247-7
; Sequence 7, Application US/08116247
; Patent No. 5929212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.

APPLICANT: Zivim, Robert A.
 APPLICANT: Adair, John R.
 APPLICANT: Atchwal, Diljeet S.
 TITLE OF INVENTION: CDS Specific Recombinant Antibody
 NUMBER OF SEQUENCES: 29
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Woodcock Masburn Kurtz Mackiewicz & No. 59292121RIS
 STREET: One Liberty Place - 46th Floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/116,247
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/743,377
 FILING DATE: 10-OCT-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Painlin, Francis A.
 REGISTRATION NUMBER: 19,386
 REFERENCE/DOCKET NUMBER: CARP-0011
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 468 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-116-247-7

Query Match	70.4%;	Score 574.5;	DB 2;	Length 468;
Best Local Similarity	74.8%;	Pred. No. 4e+0;		
Matches 113;	Conservative	8;	Mismatch 29;	Indels 1; Gaps 1
QY	1	MECSWVEFLISITTVGHSAAYLQOQSAEALVRSASVSKSCASGYTLTSMYHWKQRP	60	
Db	1	MERHMFILLISLVTAQVHSQYQLQOQSAELARFGASVSKSCASGYTLFRYTMHWKRP	60	
QY	61	GOGLEKINGIPNGNDITYNOKFKGKSLADITSSSTAYMOISLTSSEDSAVYFCAR-GN	119	
Db	61	GOGLEKIGTINRSKRYTNMOKFDKATLTITDKSSSTAYMOISLTSSEDSAVYCARYYD	120	
QY	120	MEGALDYMGQGSVTVSSAKTTPPVYPLTP	150	
Db	121	DHYCLDYMGQGTTLTVSSAKTTPAVYPLAP	151	

RESULT 4
US-09-795-515-7
Sequence 7, Application US/09795515
Patent No. 6632927
GENERAL INFORMATION:
APPLICANT: Adair, John R.
APPLICANT: Ahtwal, Diljeet S.
APPLICANT: Emrage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6632927xis
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103


```

XX PF 19-DEC-1996; 96WO-US020757.
XX PR 20-DEC-1995; 95US-00575762.
XX PR 26-JAN-1996; 96US-00591965.
XX PR 13-DEC-1996; 96US-00766350.
XX PA (KENT ) UNIV KENTUCKY.
XX PI Chatterjee M, Foon KA, Chatterjee SK;
XX DR WPI; 1997-341690/31.
XX DR N-PSDB; AAT85150.
XX PT Monoclonal anti-idiotypic antibody 11D10 - elicits immune response against
XX PT human milk fat globule disease associated tumours, especially breast
XX PT cancer.
XX PS Claim 10; Page 94-95; 130pp; English.
XX CC This polypeptide sequence comprises the heavy chain variable region (VH)
XX CC of monoclonal anti-idiotypic antibody 11D10 produced by hybridoma cell
XX CC line ATCC 12020. 11D10 was obtained by immunising naive mice with MC-10
XX CC anti-HMG antibody to obtain an anti-idiotypic response. It elicits an
XX CC immune response against a specific epitope of a high mol.wt. mucin of
XX CC human milk fat globule (HMG). It induces an immunological response to
XX CC HMG in mice, rabbits, monkeys and patients with advanced HMG-associated
XX CC tumours. Pharmaceutical compositions and vaccines comprising 11D10, 11D10
XX CC polypeptides and/or 11D10 polynucleotides (see also AAT85149-50) are
XX CC claimed. Also claimed are diagnostic kits and methods of using 11D10,
XX CC 11D10 polypeptides and/or 11D10 polynucleotides, including methods of
XX CC treating HMG-associated tumours. 11D10 is also used in a claimed method
XX CC of palliating HMG-associated disease and in claimed kits to detect or
XX CC quantify anti-HMG antibody. (Updated on 25-MAR-2003 to correct FR
XX CC field.)
XX SQ Sequence 153 AA;
XX
Query Match 100.0%; Score 816; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.1e-54;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MECSWVFLFLSLTTGVSQAYLQSGAEIVRSASVSKSCASGYTLTSTNMHWKQTP 60
DB 1 MECSWVFLFLSLTTGVSQAYLQSGAEIVRSASVSKSCASGYTLTSTNMHWKQTP 60
QY 61 GQGLEWIGNIFPGNGDTYYNOKFKKASLTADTSSSTAYMOISLTSBDSAVYFCARGNW 120
DB 61 GQGLEWIGNIFPGNGDTYYNOKFKKASLTADTSSSTAYMOISLTSBDSAVYFCARGNW 120
QY 121 EGALDYMGGTSTVTSASAKTTPPPYPLVPGSL 153
DB 121 EGALDYMGGTSTVTSASAKTTPPPYPLVPGSL 153
RESULT 2
AAW87594
ID AAW87594 standard; protein; 153 AA.
AC AAW87594;
XX
DT 16-MAR-1999 (first entry)
XX
DE Antibody 11D10 heavy chain variable region.
XX
KV Murine; mouse; antibody; heavy chain; variable region; anti-idiotypic;
XX human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
OS Mus sp.
XX
XX Key Location/Qualifiers
XX FH 1..19
XX FT Peptide /note= "signal peptide"

```

```

FT Protein 20..153
FT /note= "mature protein"
FT Region 20..49
FT /label= framework_1
FT Domain 50..54
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 55..68
FT /label= framework_2
FT Domain 69..85
FT /label= CDR2
FT Region 86..117
FT /label= framework_3
FT Domain 118..126
FT /label= CDR3
FT /note= "complementarity determining region 3"
FT Region 127..137
FT /label= framework_4
XX
XX WO956419-A1.
XX 17-DEC-1998.
XX
XX 12-JUN-1998; 98WO-US012250.
XX
XX 13-JUN-1997; 97US-0049540P.
XX 11-JUN-1998; 98US-00096244.
XX
XX (KENT ) UNIV KENTUCKY RES FOUND.
XX
XX Chatterjee M, Foon KA;
XX WPI; 1999-060029/05.
XX DR N-PSDB; AAV83773.
XX
XX Delaying development of, or treating, HMG-associated tumours - using
XX anti-idiotypic antibody 11D10 raised against antibodies to human milk fat
XX globule protein.
XX
XX Disclosure; Fig 2; 54pp; English.
XX
XX This sequence represents the heavy chain variable region of the murine
XX antibody 11D10. This anti-idiotypic antibody is used to delay the
XX development of, or treat, a human milk fat globule (HMG) associated
XX tumour in an individual having low tumour burden. The antibody 11D10 is
XX used to prevent the recurrence of HMG-associated tumours e.g. ovarian,
XX breast tumours
XX
XX Sequence 153 AA;
XX
Query Match 100.0%; Score 816; DB 2; Length 153;
Best Local Similarity 100.0%; Pred. No. 1.1e-54;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MECSWVFLFLSLTTGVSQAYLQSGAEIVRSASVSKSCASGYTLTSTNMHWKQTP 60
DB 1 MECSWVFLFLSLTTGVSQAYLQSGAEIVRSASVSKSCASGYTLTSTNMHWKQTP 60
QY 61 GQGLEWIGNIFPGNGDTYYNOKFKKASLTADTSSSTAYMOISLTSBDSAVYFCARGNW 120
DB 61 GQGLEWIGNIFPGNGDTYYNOKFKKASLTADTSSSTAYMOISLTSBDSAVYFCARGNW 120
QY 121 EGALDYMGGTSTVTSASAKTTPPPYPLVPGSL 153
DB 121 EGALDYMGGTSTVTSASAKTTPPPYPLVPGSL 153
RESULT 3
AAO16293
ID AAO16293 standard; protein; 153 AA.
XX

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 13:38:19 ; Search time 2367.26 Seconds
(without alignments)
7096.283 Million cell updates/sec

Title: US-08-836-455-3

Perfect score: 461
Sequence: 1 ATGGAATGACCTGGCTCTT.....CTGTCTCTGGAAGCTTGCG 461

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST: *
1: gb_esc1: *
2: gb_esc2: *
3: gb_esc3: *
4: gb_esc4: *
5: gb_esc5: *
6: gb_esc6: *
7: gb_esc7: *
8: gb_esc8: *
9: gb_esc9: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	337.8	73.3	739	2	BE284158 601099428
2	326.8	70.9	892	4	BG518664 602578528
3	326.6	70.8	637	6	BY724721 601781314
4	320.8	69.6	941	2	BF138189 601781314
5	320.2	69.5	667	6	BY724790 601781314
6	319.6	69.3	1576	3	AK007918 Mus muscu
7	316.6	68.7	767	2	BF165456 60177347
8	316.4	68.6	794	4	BF150371 602915205
9	315.6	68.5	745	4	BG871607 602790090
10	311.2	67.5	546	6	CA576594 K0647806-
11	310.6	67.4	771	2	BF140551 60178584
12	309.6	67.2	529	6	CA576389 K064412-
13	308.6	66.9	616	2	BF136295 601781413
14	308.4	66.9	748	2	BF136397 601783927
15	308.4	66.9	838	7	COS55369 AGENCOURT
16	308.6	66.8	755	7	CF912433 A0632A03-
17	306.6	66.5	700	2	BF540088 602050325
18	305.6	66.2	644	2	BE281961 601098518
19	305	66.2	793	2	BF136093 601785539
20	305	66.2	891	2	BF138460 601782916
21	303.4	65.8	756	7	COS58337 AGENCOURT
22	303	65.7	955	7	BQ947728 AGENCOURT
23	302.6	65.6	469	6	CA574907 K0622H02-
24	301.6	65.4	690	4	BG966862 602836513

25	301.6	65.4	724	4	BG962137 602826902
26	301.4	65.4	753	7	COS59221 AGENCOURT
27	300.4	65.2	767	7	COS5860 AGENCOURT
28	299.8	65.0	604	2	BF140035 601791175
29	298.4	64.7	538	6	CA578968 K0731A04-
30	297.4	64.5	540	6	CA579750 K0741H07-
31	296.8	64.4	610	7	CF912857 A0638H09-
32	296.8	64.4	724	2	BF168514 601775412
33	296.8	64.4	847	2	BF165486 601773393
34	296.2	64.3	507	2	BF015548 UY23A08.Y
35	295.8	64.2	519	6	CA580087 K0746G01-
36	295.2	64.0	769	2	BF168856 601775314
37	293.6	63.7	819	4	BG966397 602832896
38	293	63.6	477	6	CA570382 K0505G11-
39	293	63.6	612	7	CN661462 A0719E06-
40	292.8	63.5	640	5	BQ109114 ImageQC_6
41	292.6	63.5	465	6	CA578116 K0718G11-
42	292.4	63.4	475	6	CA578534 K0725B11-
43	292.4	63.4	646	7	CN662544 A0735E04-
44	292.2	63.4	911	2	BE286958 601092470
45	292	63.3	429	6	CA579143 K0733D01-

ALIGNMENTS

RESULT 1
LOCUS BE284158 739 bp mRNA linear EST 13-JUL-2000
DEFINITION 601099428F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3491766 5',
RNA sequence.
ACCESSION BE284158 GI:9160900
VERSION BE284158.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE NIH (bases 1 to 739)
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: L1AM8536 row: h column: 07
High quality sequence stop: 535.

FEATURES

source 1..739
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3491766"
/tissue_type="spontaneous tumor, metastatic to mammary."
Stem cell origin.
/lab_host="DHI08"
/clone_id="NCI CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI; Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 73.3%; Score 337.8; DB 2; Length 739;
Best Local Similarity 84.1%; Pred. No. 9,6e-90;
Matches 301; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 15:14:29 ; Search time 687.898 Seconds
(without alignments)
3682.388 Million cell updates/sec

Title: US-08-836-455-3

Perfect score: 461
Sequence: 1 ATGGAATGACGCTGGCTTT.....CTGGTCCTGGAAGCTTGCG 461

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3694831 seqs, 2747406616 residues

Total number of hits satisfying chosen parameters: 7389662

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	461	9	US-09-861-294-3 Sequence 3, Appl1
2	461	100.0	461	15	US-10-367-506-3 Sequence 3, Appl1
3	337.8	73.3	1406	18	US-10-742-405-11 Sequence 11, Appl1
4	327.2	71.0	409	14	US-10-160-232-7 Sequence 7, Appl1
5	326.6	70.8	736	13	US-10-006-773-12 Sequence 12, Appl1
6	311.6	67.2	1570	17	US-10-682-845-39 Sequence 39, Appl1
7	310	67.2	1570	10	US-09-793-515-6 Sequence 6, Appl1
8	310	67.2	1570	16	US-10-704-352-6 Sequence 6, Appl1
9	310	67.2	1570	18	US-10-703-963-6 Sequence 6, Appl1
10	297.2	64.5	9199	10	US-09-911-692-3 Sequence 3, Appl1
11	297.2	64.5	9209	9	US-09-911-703-3 Sequence 3, Appl1
12	297.2	64.5	9209	10	US-09-905-928-2 Sequence 2, Appl1

13	297.2	64.5	9209	14	US-10-096-964-2	Sequence 2, Appl1
14	297.2	64.5	9209	15	US-10-238-681-3	Sequence 3, Appl1
15	297.2	64.5	9209	16	US-10-411-037-58	Sequence 58, Appl1
16	297.2	64.5	9209	16	US-10-411-026-58	Sequence 58, Appl1
17	297.2	64.5	9209	16	US-10-410-962-58	Sequence 58, Appl1
18	297.2	64.5	9209	16	US-10-411-049-58	Sequence 58, Appl1
19	297.2	64.5	9209	17	US-10-410-930-58	Sequence 58, Appl1
20	297.2	64.5	9209	17	US-10-410-997-58	Sequence 58, Appl1
21	297.2	64.5	9209	17	US-10-411-012-58	Sequence 58, Appl1
22	297.2	64.5	9209	17	US-10-287-994-58	Sequence 58, Appl1
23	297.2	64.5	9209	17	US-10-410-913-58	Sequence 58, Appl1
24	297.2	64.5	18986	13	US-10-109-853-2	Sequence 2, Appl1
25	297.2	64.5	18986	17	US-10-817-956-2	Sequence 2, Appl1
26	296.4	64.3	1392	15	US-10-216-484-8	Sequence 8, Appl1
27	296.4	64.3	1392	15	US-10-384-933-8	Sequence 8, Appl1
28	295.2	64.0	482	9	US-09-881-823-19	Sequence 19, Appl1
29	292	63.3	478	13	US-10-040-739-911	Sequence 911, App
30	291.4	63.2	1314	9	US-09-903-327A-5	Sequence 5, Appl1
31	291.4	63.2	1516	9	US-09-753-436-77	Sequence 1, Appl1
32	289.6	62.8	422	9	US-10-163-942-77	Sequence 77, Appl1
33	289.6	62.8	422	15	US-10-163-942-77	Sequence 77, Appl1
34	289.2	62.7	406	15	US-10-150-762-85	Sequence 85, Appl1
35	289.2	62.7	406	15	US-10-150-762-85	Sequence 85, Appl1
36	289.2	62.7	406	15	US-10-244-821-85	Sequence 85, Appl1
37	287.4	62.3	519	17	US-10-642-120-1	Sequence 1, Appl1
38	287.4	62.3	519	17	US-10-642-060-1	Sequence 1, Appl1
39	287.4	62.3	519	17	US-10-642-122-1	Sequence 1, Appl1
40	287.4	62.3	519	17	US-10-642-124-1	Sequence 1, Appl1
41	287.4	62.3	519	17	US-10-621-269-1	Sequence 1, Appl1
42	287.4	62.3	519	17	US-10-620-850-1	Sequence 1, Appl1
43	287.4	62.3	519	18	US-10-642-118-1	Sequence 1, Appl1
44	287.4	62.3	519	18	US-10-642-117-1	Sequence 1, Appl1
45	287.4	62.3	519	18	US-10-642-119-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1
US-09-861-294-3
; Sequence 3, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 461
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(461)
; NAME/KEY: sig_peptide
; LOCATION: (1)...(57)
; NAME/KEY: mat_peptide
; LOCATION: (58)...(461)
US-09-861-294-3

Query Match 100.0%; Score 461; DB 9; Length 461;
Best Local Similarity 100.0%; Pred. No. 5.1e-140;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ATGAAATGCACTGGGCTTTCTCTTCTCTCTGCAATTAATCAAGGTGTCACCTCCAG 60

QY 61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAAGCTGGGGCTGAGGAAGATGCC 120

Db 61 GCTTATCTACAGCAGTCTGGGGCTGAGCTGGTGAAGCTGGGGCTGAGGAAGATGCC 120

QY 121 TGCAGGCTTCTGGCTACACATTGACCGATTACATATGCACTGGGTAAAGCAGACCT 180

Db 121 TGCAGGCTTCTGGCTACACATTGACCGATTACATATGCACTGGGTAAAGCAGACCT 180

QY 181 GCAAGGGCTGGAATGGAATTGGAAATTTTCTCGAAATGTTAATCTTACAAT 240

Db 181 GCAAGGGCTGGAATGGAATTGGAAATTTTCTCGAAATGTTAATCTTACAAT 240

QY 241 CAGAAGTTTAAAGGCAAGGCTCATTTAGCTGCGAGACATCTCCAGCAGGCTTCAATG 300

Db 241 CAGAAGTTTAAAGGCAAGGCTCATTTAGCTGCGAGACATCTCCAGCAGGCTTCAATG 300

QY 301 CAGATCAGAGCCTGACATCTGAAGAATCTGGGCTTATTTCTGTGCAAGAGGAACATG 360

Db 301 CAGATCAGAGCCTGACATCTGAAGAATCTGGGCTTATTTCTGTGCAAGAGGAACATG 360

QY 361 GAGGGTCTCTGAGCTTACCTGGGGTCAAGGAACCTCAGTCAACCGTCTCTCAGCAAAAG 420

Db 361 GAGGGTCTCTGAGCTTACCTGGGGTCAAGGAACCTCAGTCAACCGTCTCTCAGCAAAAG 420

QY 421 ACACCCCAACCGTCTATCTCACTGGTCCCTGGAACCTTGGG 461

Db 421 ACACCCCAACCGTCTATCTCACTGGTCCCTGGAACCTTGGG 461

RESULT 3
US-10-74

```

? Sequence 11 Application US/10742405
? Publication No. US20040213761A1
? GENERAL INFORMATION:
? APPLICANT: Bowman, Edward P.
? APPLICANT: Chan, Jason R.
? APPLICANT: Moore, Kevin
? APPLICANT: Nguyen, Nhung
? APPLICANT: Churakova, Tatyana
? APPLICANT: Chen, Shi-Juan
? APPLICANT: Cua, Daniel J.
? TITLE OF INVENTION: Uses of mammalian cytokine; related reagents
? FILE REFERENCE: DX01578K
? CURRENT APPLICATION NUMBER: US/10/742,405
? NUMBER OF SEQ ID NOS: 12
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO 11
? LENGTH: 1406
? TYPE: DNA
? ORGANISM: Mus musculus
US-10-742-405-11

```

Answer Match

[illegible]

Dib

181 GGACAGGCGCTGGAATGATTTGGAAATATTTTTCCTGGAAATGATGATACCTTACTACAAT 240

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 6, 2004, 13:29:00 ; Search time 58.0168 Seconds
(without alignments)
1517.360 Million cell updates/sec

Title: US-08-836-455-4

Perfect score: 816

Sequence: 1 MECGKVFLLSLITGVHSG.....TVSSAKTTPPVPLVPGSL 153

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database: UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trcembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	589.5	72.2	473	2	Q9DBL4
2	581	71.2	463	2	Q99LC4
3	575	70.5	465	2	Q6PUB2
4	575	70.5	465	2	AAH18280
5	569	69.7	473	2	Q99L25
6	561.5	68.8	464	2	Q6PR95
7	561.5	68.8	464	2	AAH57672
8	553.5	67.8	472	2	Q6P3A7
9	553.5	67.8	472	2	AAH18535
10	549.5	67.3	470	2	Q8VDC9
11	548.5	67.2	470	2	Q7TMM1
12	544	66.7	613	2	Q8VCK7
13	524.5	64.5	481	2	Q91WT1
14	524.5	64.3	474	2	Q8R3H6
15	523.5	64.2	140	1	HV02_MOUSE
16	521	63.8	482	2	Q8K172
17	518.5	63.5	614	2	Q7TMT6
18	516.5	63.3	489	2	Q8VCK4
19	515.5	63.2	468	2	Q99L31
20	514	63.0	136	2	Q7TPE3
21	506.5	62.1	142	2	Q924Q1
22	499	61.2	480	2	Q8K024
23	494.5	60.6	481	2	Q8VCK5
24	493	60.4	139	1	HV07_MOUSE
25	493	60.4	139	1	HV07_MOUSE
26	489	59.9	488	2	Q8K0P2
27	482	59.1	143	2	Q924R0
28	479.5	58.8	481	2	Q91WT3
29	478	58.8	145	2	Q924R4
30	477.5	58.5	464	2	AAH19337
31	474	58.1	145	2	Q924P7

ALIGNMENTS

32	474	58.1	145	2	Q924R1
33	473.5	58.0	140	2	Q924P8
34	473.5	58.0	146	2	Q924Q3
35	472	57.8	145	2	Q924Q6
36	471	57.7	143	2	Q924P9
37	470	57.6	137	1	HV11_MOUSE
38	469	57.5	145	2	Q924Q9
39	467	57.2	145	2	Q924Q7
40	466.5	57.2	142	2	Q924Q2
41	466.5	57.2	146	2	Q924R8
42	465	57.0	143	2	Q924Q0
43	464	56.9	143	2	Q924P6
44	464	56.9	143	2	Q924R7
45	464	56.9	145	2	Q924R3

RESULT 1					
Q9DBL4	PRELIMINARY;	PRT;	473	AA.	
AC	Q9DBL4;				
DT	01-JUN-2001 (TrEMBLrel. 17, Created)				
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)				
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)				
DE	Mus musculus 10 day old male pancreas cDNA, RIKEN full-length enriched library, clone:181006009 product:immunoglobulin heavy chain 6 (heavy DE chain of IgM), full insert sequence.				
GN	Name=Igh-1a;				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.				
OX	NCBI_TaxID=10090;				
OX	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;				
RC	MEDLINE=99279253; PubMed=10349636;				
RA	Carninci P.; Hayashizaki Y.;				
RT	"High-efficiency full-length cDNA cloning.";				
RL	Meth. Enzymol. 303:19-44(1999).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;				
RC	MEDLINE=21085660; PubMed=11217851;				
RA	RIKEN FANTOM Consortium;				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 409:685-690(2001).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;				
RC	The FANTOM Consortium;				
RA	the RIKEN Genome Exploration Research Group Phase I & II Team;				
RT	"Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";				
RL	Nature 420:563-573(2002).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Pancreas;				
RC	MEDLINE=2049374; PubMed=11042159;				
RA	Carninci P.; Shibata Y.; Hayatsu N.;				
RA	Kono H.; Okazaki Y.; Muramatsu M.;				
RA	Kono H.; Okazaki Y.; Muramatsu M.;				
RA	Shibata K.; Itoh M.; Aizawa K.;				
RA	Komoto H.; Akiyama J.; Nishii K.;				
RA	Sumi N.; Ishii Y.; Nakamura S.;				
RA	Yamamoto R.; Matsumoto H.;				
RA	Sakaguchi S.;				
RA	Ikegami T.;				
RA	Kashiwagi K.;				

RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashiaki Y.,
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 RL sequencing pipeline with 384 multicapillary sequencer.",
 RN Genome Res. 10:1757-1771 (2000).
 [6].

RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE=Pancreas;
 RA Adachi U., Alizawa K., Akahira S., Akimura T., Arai A., Aono H.,
 RA Arahata T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuo M.,
 RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirooka T., Hori F.,
 RA Imotani K., Ishii Y., Itoh M., Izawa M., Kankawa T., Kato H.,
 RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
 RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ono M.,
 RA Okazaki Y., Okido T., Owa C., Saito K., Saito R., Sakai K.,
 RA Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,
 RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
 RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashiaki Y.,
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AK007918; BAB5349.1; .

DR PIR; PH165; PH165.
 DR PIR; S1966; S1966.
 DR PIR; S26746; S26746.
 DR HSSP; P01864; 1BOG.
 DR MGD; MGI:96443; Igh-1a.
 DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
 DR GO; GO:0005271; C:multivesicular body; IDA.
 DR GO; GO:0003823; P:antigen binding; IDA.
 DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.
 DR GO; GO:0003033; P:antigen processing; IDA.
 DR GO; GO:0006958; P:complement activation, classical pathway; IDA.
 DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
 DR GO; GO:0006933; P:endosome to lysosome transport; IDA.
 DR GO; GO:0006910; P:phagocytosis, recognition; IDA.
 DR GO; GO:0005071; P:phagocytosis, recognition; IDA.
 DR GO; GO:0050778; P:positive regulation of B-cell activation; IDA.
 DR GO; GO:0050766; P:positive regulation of immune response; IDA.
 DR GO; GO:0001812; P:positive regulation of phagocytosis; IDA.
 DR GO; GO:0001981; P:positive regulation of type I hypersensitivity; IDA.
 DR GO; GO:0001798; P:positive regulation of type I hypersensitivity; IDA.
 DR GO; GO:0030162; P:regulation of proteolysis and peptidolysis; IDA.
 DR InterPro; IPR007110; Igh-1like.
 DR InterPro; IPR003597; Igh_c1.
 DR InterPro; IPR003006; Igh_MHC.
 DR InterPro; IPR003596; Igh_v.
 DR Pfam; PF07654; C1-sect_3.
 DR Pfam; PF00047; Igh_1.
 DR SMART; SM00406; Igh_1.
 DR PROSITE; PS0835; Igh_LIKE; 4.
 DR PROSITE; PS00290; Igh_MHC; UNKNOWN 1.
 SQ SEQUENCE 473 AA; 51699 MW; 9DEB57A514475FBB CRC64;

Query Match 72.2%; Score 589.5; DB 2; Length 473;
 Best local Similarity 74.8%; Pred. No. 2,1e-45;
 Matches 113; Conservative 13; Mismatches 24; Indels 1; Gaps 1;
 QY 1 MECSWVFLLSLITGVHSAVLIQSGALVSGASVKNKSGAVTLLTSYMHVKKOTP 60
 DB 1 MEMSWVFLLSLITGVHSAVLIQSGALVSGASVKNKSGAVTLLTSYMHVKKOTP 60
 QY 61 GGGLEWIGIGIGSGSYTYNEKFKATLTDKSSSTAYMOISLTSBDSAVYFCARGNW 120
 DB 61 GGGLEWIGIGIGSGSYTYNEKFKATLTDKSSSTAYMOISLTSBDSAVYFCARGNW 120
 QY 121 E-GALDYMGGTSVYVSAKTTTPPVYPLVP 150
 DB 121 DYDWFAYMGQGLTVVSAKTTAASVYPLAP 151

RESULT 2
 Q99LC4

ID Q99LC4 PRELIMINARY; PRT; 463 AA.

AC Q99LC4;

DT 01-JUN-2001 (T-EMBLrel. 17, Created)

DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)

DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

DE Igh-4 protein.

GN Name=Igh-4;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N;

RC TISSUE=Mammary tumor. Metallochromien-TGF alpha model. 10 month old

RC virgin mouse. Taken by biopsy.

RX MEDLINE=22386257; PubMed=12477932;

RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.L., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Burow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant J.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshnyuk S., Carninci P., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smallos D.E., Scherch A., Schein J.E.,

RA Jones S.J., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=FVB/N;

RC TISSUE=Mammary tumor. Metallochromien-TGF alpha model. 10 month old

RC virgin mouse. Taken by biopsy.

RA Strausberg R.,

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC003435; AAH03435.1; .

DR PIR; B45837; B45837.

DR HSSP; P01869; 1CL7.

DR MGD; MGI:96446; Igh-4.

DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.

DR GO; GO:0003823; P:antigen binding; IDA.

DR GO; GO:0019723; P:antibacterial humoral response (sensu Verte. . . IDA.

DR GO; GO:0001788; P:antibody-dependent cellular cytotoxicity; IDA.

DR GO; GO:0006958; P:complement activation, classical pathway; IDA.

DR GO; GO:0004911; P:defense response to pathogenic bacteria; IDA.

DR GO; GO:0006910; P:phagocytosis, engulfment; IDA.

DR GO; GO:0050778; P:positive regulation of immune response; IDA.

DR GO; GO:0050766; P:positive regulation of immune response; IDA.

DR GO; GO:0001812; P:positive regulation of phagocytosis; IDA.

DR GO; GO:0001798; P:positive regulation of type I hypersensitivity; IDA.

DR InterPro; IPR007110; Igh-1like.

DR InterPro; IPR003597; Igh_c1.

DR InterPro; IPR003006; Igh_MHC.

DR InterPro; IPR003596; Igh_v.

DR Pfam; PF07654; C1-sect_3.

DR Pfam; PF00047; Igh_1.

DR SMART; SM00406; Igh_1.

DR PROSITE; PS0835; Igh_LIKE; 4.

DR PROSITE; PS00290; Igh_MHC; UNKNOWN 1.

SQ SEQUENCE 463 AA; 51007 MW; EAA674C6B8C30783 CRC64;

Query Match 71.2%; Score 581; DB 2; Length 463;
 Best local Similarity 70.8%; Pred. No. 1.2e-44;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2004, 13:29:00 ; Search time 15.4027 Seconds

(without alignments)
955.753 Million cell updates/sec

Title: US-08-836-455-4

Perfect score: 816
Sequence: 1 MECSWVFLFLSLITGVHSQ.....TVSSAKTTPPPVPLVPSL 153Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: PIR79:.*
2: PIR1:.*
3: PIR2:.*
4: PIR4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	568	69.6	475	2 S01321	Ig gamma-2b chain
2	563	69.0	469	2 S37483	Ig gamma-2a chain
3	560	68.6	474	1 G2MS11	Ig gamma-2b chain
4	549	67.3	139	2 PS0024	Ig heavy chain pre
5	548.5	67.2	151	2 PL0011	Ig heavy chain pre
6	547	67.0	150	2 PN0444	Ig heavy chain V r
7	537.5	65.9	246	2 S38950	Ig gamma chain - m
8	537.5	65.9	446	2 S40295	Ig gamma-2a chain
9	533	65.3	178	2 S29594	Ig gamma chain (NM
10	529	64.8	137	2 H32513	Ig heavy chain pre
11	527.5	64.6	140	2 PH1482	Ig heavy chain V r
12	523.5	64.2	140	1 HVM57	Ig heavy chain pre
13	523.5	64.2	166	2 PL0012	Ig heavy chain pre
14	516.5	63.3	140	2 PH1489	Ig heavy chain V r
15	512	62.7	141	2 A39276	Ig heavy chain pre
16	510.5	62.6	138	2 E32513	Ig heavy chain pre
17	507.5	62.2	138	2 S21810	Ig heavy chain V r
18	507	62.1	133	2 PC1155	Ig heavy chain pre
19	506.5	62.1	140	2 PH1488	Ig heavy chain V r
20	502.5	61.6	135	2 PH1493	Ig heavy chain V r
21	502.5	61.6	140	2 PH1498	Ig heavy chain V r
22	502.5	61.6	140	2 PH1494	Ig heavy chain V r
23	501.5	61.2	135	2 PS0057	Ig heavy chain pre
24	499	60.9	139	2 A27609	Ig heavy chain pre
25	497	60.8	135	2 PH1492	Ig heavy chain V r
26	496.5	60.7	135	2 A30577	Ig heavy chain pre
27	495	60.6	140	2 PH1486	Ig heavy chain V r
28	494.5	60.4	139	1 MHMS18	Ig heavy chain pre
29	493				

30	491.5	60.2	136	2 PL0208	Ig heavy chain pre
31	491.5	60.2	140	2 A36194	Ig heavy chain V r
32	490	60.0	141	2 JL0076	Ig heavy chain pre
33	487.5	59.7	140	2 PH1483	Ig heavy chain V r
34	484.5	59.4	140	2 T01407	Ig heavy chain (my
35	480	58.8	214	2 PC4202	monoclonal antibody
36	479.5	58.8	140	2 S04575	Ig heavy chain pre
37	476	58.3	171	2 S23523	Ig heavy chain V r
38	472.5	57.9	136	2 S04576	Ig heavy chain pre
39	472	57.8	137	2 F29380	Ig heavy chain V r
40	470.5	57.7	140	2 PH1499	Ig heavy chain V r
41	470	57.6	117	2 S03289	Ig heavy chain pre
42	470	57.6	136	2 JL0077	Ig heavy chain pre
43	470	57.6	137	1 G2MS43	Ig heavy chain pre
44	468	57.4	137	2 E29380	Ig heavy chain pre
45	467.5	57.3	121	2 A26405	Ig heavy chain V r

ALIGNMENTS

```
RESULT 1
S01321
Ig gamma-2b chain precursor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C/Accession: S01321
R/de Waale, P.; Fey, V.; van de Voerde, A.; Mollema, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A/Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed
A/Reference number: S01320; MID:88329081; PMID:3138116
A/Accession: S01321
A/Molecule type: mRNA
A/Residues: 1-475 <DE1>
A/Cross-references: EMBL:X13188; NID:G51780; PID:CAA1580.1; PID:G51781
A/Note: this sequence was determined from the differentiated gene
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: immunoglobulin
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-475/Product: Ig gamma-2b chain #status predicted <MAT>
F/159-223/Domain: immunoglobulin homology <IMM>

Query Match          69.6% Score 568; DB 2; Length 475;
Best Local Similarity 71.2% Pred. No. 1e-37;
Matches 109; Conservative 14; Mismatches 28; Indels 2; Gaps 1;

QY      1 MECSWVFLFLSLITGVHSQAYLQSGAEIVREGASVKNKSKAGYTLTSMHMYKQP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MEWIVFLFLSLITGVHSQAYLQSGAEIVREGASVKNKSKAGYTLTSMHMYKQP 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      61 GQLEWIGNIFPQNGDTYNNQKFKASLTADTSSTAYWQISLTSBDSAVYFCARGNW 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 GQLEWIGNIFPQNGDTYNNQKFKASLTADTSSTAYWQISLTSBDSAVYFCARGNW 120
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY      121 EGNL--DYWGQGTSTVVSNAKTPPPVPLVPSL 151
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 VGLLPFGWGGTLVTASAKTTPPSVYPLAPG 153
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
S37483
Ig gamma-2a chain - mouse
C/Species: Mus musculus (house mouse)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37483
R/Duncan, P.F.D.
submitted to the EMBL Data Library, February 1993
A/Reference number: S37483
A/Accession: S37483
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-469 <DUC>
A/Cross-references: EMBL:X70423; NID:G406252; PID:CAA49868.1; PID:G406253
```

C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 563; DB 2; Length 469;
Best Local Similarity 71.7%; Pred. No. 2, 5e-37;
Matches 109; Conservative 15; Mismatches 26; Indels 2; Gaps 1;

```

QY 1 MECSWVFLFLSITTTGVHSAVYLQOSGAEIVRSASVMSCKASGYTLTSYMHVVKQTP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEMSWIFFLFSLGTAGVHCOQLQOSGPELVKPGASVMSCKASGYTLTDYIMVWVKQRP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 GGGLEWIGNIFPFGNDITYNOKFKKASLTADTSSSTAYMOISLTSSEDSAVYFCAR--G 118
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GGGLEWIGNIVASNTYKNEFKKATLTVDTSSTAYMOISLTSSEDSAVYFCARAG 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 119 NMEGALDYGQGTSTVSSAKTTPPPVPLVP 150
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 ATATLLDYGQGTTLTVSSAKTAPSVPLAP 152
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

RESULT 3

G2MS11

Ig gamma-2b chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1980 #sequence revision 01-Dec-2000 #text change 09-Jul-2004

C:Accession: S25057; A02157; A26232; A26233; A53558

R: Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.-J.; Kreuzaler, F.

submitted to the EMBL Data Library, July 1992

A:Description: Production of a tobacco mosaic virus (TMV) inactivating neotop specific

A:Reference number: S25057

A:Accession: S25057

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-474 <PIS>

A:Cross-references: UNIPROT:P01866; EMBL:X67210; NID:954826; PIDN:CAA47649.1; PID:954827

R: Yamawaki-Karaoke, Y.; Katooka, T.; Takahashi, N.; Obata, M.; Honjo, T.

Nature 283, 786-789, 1980

A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from

A:Reference number: A02157; MUID:80120716; PMID:6766534

A:Contents: a allele

A:Molecule type: DNA

A:Residues: 138-161, 'L', 163-189, 'P', 193-474 <YAM>

A:Cross-references: GB:000461

A:Note: the sequence was determined from the germline gene

R: Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.

Science 206, 1299-1303, 1979

A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b

A:Reference number: A26235; MUID:80081501; PMID:117548

A:Contents: MPC 11

A:Accession: A26235

A:Molecule type: mRNA

A:Residues: 138-172, 'P', 174-189, 'P', 193-376, 'T', 378-474 <TU2>

R: O'Neil, R.; Rougeon, F.

Nature 296, 761-763, 1982

A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma

A:Reference number: A26233; MUID:82173203; PMID:6803173

A:Contents: b allele

A:Accession: A26233

A:Molecule type: DNA

A:Residues: 138-161, 'L', 163-189, 'P', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OIL>

A:Cross-references: GB:J00461

R: Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi

J. Biol. Chem. 269, 12343-12350, 1994

A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A:Reference number: A53598; MUID:94216359; PMID:7512967

A:Accession: A53598

A:Status: Preliminary

A:Molecule type: protein

A:Residues: 234-251 <KIM>

C:Comment: The a allele sequence is shown.

C:Genetics:

A:Introns: 138/1, 236/1; 258/1, 368/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (k)

chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob

F:157-222/Domain: immunoglobulin homology <IM1>

F:236-257/Region: hinge

F:281-350/Domain: immunoglobulin homology <IM2>

F:387-454/Domain: immunoglobulin homology <IM3>

F:152/Disulfide bonds: interchain (to light chain) #status predicted

F:164-220,288-348,394-452/Disulfide bonds: #status predicted

F:247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted

F:324/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match

68.6%; Score 560; DB 1; Length 474;

Best Local Similarity 70.8%; Pred. No. 4, 4e-37;

Matches 109; Conservative 13; Mismatches 26; Indels 6; Gaps 2;

```

QY 1 MECSWVFLFLSITTTGVHSAVYLQOSGAEIVRSASVMSCKASGYTLTSYMHVVKQTP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MEMSWIFFLFSLGTAGVHSEVQLQOSGPELVKPGASVMSCKASGYTLTDYIMVWVKQRP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 GGGLEWIGNIFPFGNDITYNOKFKKASLTADTSSSTAYMOISLTSSEDSAVYFCAR-- 118
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GGGLEWIGNIVPNKDTKFNKFKKATLTSSSNAYMELSLTSSEDSAVYFCARDYD 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 119 NMEGALDYGQGTSTVSSAKTTPPPVPLVP 151
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 YDM--FAFMGQGLTVSSAKTTPPSVPLAPG 151
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

RESULT 4

PS0024

Ig heavy chain precursor V region (6A4) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 07-Jun-1990 #sequence revision 07-Jun-1990 #text change 22-Nov-1996

C:Accession: PS0024

R: Margel, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Dondey, H.

Gene 74, 335-345, 1988

A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains of

A:Reference number: PS0023; MUID:89232725; PMID:3149944

A:Accession: PS0024

A:Molecule type: mRNA

A:Residues: 1-139 <MAR>

A:Experimental source: strain BALB/c

C:Comment: This chain is obtained from an IgG2a monoclonal antibody against Pseudomonas

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-119/Domain: Ig heavy chain V region #status predicted <IGV>

F:34-117/Domain: immunoglobulin homology <IMV>

F:20/Modified site: pyroglutamic acid (Gln) (in mature form) #status predicted

Query Match 67.3%; Score 549; DB 2; Length 139;

Best Local Similarity 76.3%; Pred. No. 8, 8e-37;

Matches 106; Conservative 9; Mismatches 22; Indels 2; Gaps 1;

```

QY 1 MECSWVFLFLSITTTGVHSAVYLQOSGAEIVRSASVMSCKASGYTLTSYMHVVKQTP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MEMSWIFFLFSLGTAGVHSAVYLQOSGAEIVRSASVMSCKASGYTLTDYIMVWVKQRP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 61 GGGLEWIGNIFPFGNDITYNOKFKKASLTADTSSSTAYMOISLTSSEDSAVYFCAR-- 118
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 GGGLEWIGNIVNTYTYENONFKDKATLTADKSSSTAYMOISLTSSEDSAVYFCARSY 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

GenCore Version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 13:38:54 ; Search time 66.8662 Seconds
(without alignments)
4898.976 Million cell updates/sec

Title: US-08-836-455-3

Perfect score: 461
Sequence: 1 ATGGAATGACGCTGGCTTT.....CTGCTCCCTGGAAGCTTGGG 461

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	461	3	US-09-096-244-3
2	324.6	70.4	453	4	US-08-513-968-33
3	322	69.8	459	4	US-09-724-138-43
4	320	69.4	1683	3	US-09-192-545-1
5	311.6	67.6	1570	2	US-08-116-247-6
6	311.6	67.6	1570	4	US-09-348-224-6
7	310	67.2	1570	2	US-08-303-5698-6
8	310	67.2	1570	4	US-09-795-515-6
9	304.4	66.0	1572	4	US-08-353-400-23
10	299.8	65.0	1421	4	US-09-254-180C-142
11	297.2	64.5	9209	1	US-08-149-099C-3
12	297.2	64.5	9209	1	US-08-476-275-2
13	297.2	64.5	9209	2	US-08-478-967A-3
14	297.2	64.5	9209	4	US-08-475-815B-3
15	297.2	64.5	9209	4	US-08-475-813-2
16	297.2	64.5	18986	2	US-08-819-866-2
17	297.2	64.5	18986	2	US-09-023-715-2
18	297.2	64.5	18986	4	US-09-343-485A-2
19	297	64.4	10844	3	US-08-444-644-41
20	297	64.4	10844	3	US-08-232-246A-41
21	295.8	64.2	408	5	PCT-US93-11611-3
22	295.4	64.1	10785	3	US-08-444-644-27
23	295.4	64.1	10785	3	US-08-232-246A-27
24	295.4	64.1	11528	3	US-08-444-644-18
25	295.4	64.1	11528	3	US-08-232-246A-18
26	294.2	63.8	417	2	US-08-452-164A-7
27	293.2	63.6	416	1	US-08-253-877C-7

28	293.2	63.6	416	3	US-08-603-024-1	Sequence 1, Appl1
29	293.2	63.6	416	2	US-08-450-809-1	Sequence 1, Appl1
30	291	63.1	411	2	US-08-574-699A-3	Sequence 3, Appl1
31	289.6	62.8	422	1	US-08-482-882-77	Sequence 77, Appl1
32	289.6	62.8	422	1	US-08-483-389-77	Sequence 77, Appl1
33	289.6	62.8	422	2	US-08-487-113D-77	Sequence 77, Appl1
34	289.6	62.8	422	2	US-08-473-503-77	Sequence 77, Appl1
35	289.6	62.8	422	2	US-08-483-932-77	Sequence 77, Appl1
36	289.6	62.8	422	2	US-08-720-420A-77	Sequence 77, Appl1
37	289.6	62.8	422	3	US-08-714-017-77	Sequence 77, Appl1
38	289.6	62.8	422	3	US-08-475-680-77	Sequence 77, Appl1
39	289.6	62.8	1425	4	US-09-592-998C-6	Sequence 6, Appl1
40	288.4	62.6	690	2	US-08-634-783A-1	Sequence 1, Appl1
41	288.4	62.6	690	3	US-09-070-817-1	Sequence 1, Appl1
42	286.6	62.2	405	1	US-07-634-278-68	Sequence 68, Appl1
43	286.6	62.2	405	1	US-08-477-728-68	Sequence 68, Appl1
44	286.6	62.2	405	1	US-08-474-040-68	Sequence 68, Appl1
45	286.6	62.2	405	1	US-08-487-200-68	Sequence 68, Appl1

ALIGNMENTS

RESULT 1
US-09-096-244-3
Sequence 3, Application US/09096244
Patent No. 6274143
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
APPLICANT: Foon, Kenneth A.
TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
TITLE OF INVENTION: HMGs-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 11D10
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,244
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Polizzi, Catherine M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 30414-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 913-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..459
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 58
US-09-096-244-3
Query Match 100.0%; Score 461; DB 3; Length 461;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 13:36:24 ; Search time 352.953 Seconds
(without alignments)
6856.387 Million cell updates/sec

Title: US-08-836-455-3

Perfect score: 461
Sequence: 1 ATGGAATGACGCTGGCTCTT.....CTGCTCCCTGGAAGCTTGGG 461

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: genebegn19808:*
2: genebegn19808:*
3: genebegn20008:*
4: genebegn20018:*
5: genebegn20018:*
6: genebegn20028:*
7: genebegn20028:*
8: genebegn20038:*
9: genebegn20038:*
10: genebegn20038:*
11: genebegn20038:*
12: genebegn20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	461	2	AAT85150
2	461	100.0	461	2	AAV83773
3	461	100.0	461	8	AAU51274
4	337.6	73.2	1401	9	AAU58178
5	327.2	71.0	409	3	AAZ87715
6	327.2	71.0	409	4	AAZ87715
7	326.6	70.8	726	8	ABX16571
8	323	70.1	540	1	AAU91645
9	322	69.8	458	1	AAU91146
10	322	69.8	459	2	AAU82357
11	322	69.8	459	4	AAU82357
12	322	69.8	459	10	AAU82357
13	322	69.8	491	2	AAU70868
14	322	69.8	491	2	AAU70868
15	322	69.8	491	2	AAU70868
16	322	69.8	491	2	AAU70868
17	322	69.8	491	2	AAU70868
18	322	69.8	491	2	AAU70868
19	320.6	69.5	520	2	AAU70868
20	320	69.4	520	2	AAU70868
21	314.8	68.3	494	2	AAU70868

22	311.6	67.6	1570	2	AAU12637	AaU12637 Monoclonal
23	311.6	67.6	1570	12	AAU12637	AaU12637 Monoclonal
24	310.2	67.3	1581	1	AAU48037	AaU48037 Monoclonal
25	309.4	67.1	459	1	AAU70971	AaU70971 2H7 VH se
26	308.6	66.9	420	1	AAU81910	AaU81910 Anti-CA12
27	308.2	66.9	588	2	AAU43385	AaU43385 H-chain V
28	308.2	66.9	1392	2	AAU62935	AaU62935 3F4 (Chim
29	308.2	66.9	1395	2	AAU62935	AaU62935 Murine an
30	308.2	66.9	3400	2	AAU62937	AaU62937 3F4 human
31	308.2	66.9	5300	2	AAU62938	AaU62938 3F4 human
32	306.4	66.5	468	2	AAU05544	AaU05544 Nucleotid
33	305	66.2	725	3	AAU43821	AaU43821 Mouse sec
34	304.4	66.0	1582	2	AAU94037	AaU94037 Mab 55.1
35	299.8	65.0	440	2	AAU22074	AaU22074 DNA encod
36	299	64.9	458	2	AAU15164	AaU15164 VH186 reg
37	297.4	64.5	1773	2	AAU88869	AaU88869 H chain s
38	297.4	64.5	1773	2	AAU66735	AaU66735 Anti-huma
39	297.4	64.5	1773	3	AAU78202	AaU78202 Anti-huma
40	297.2	64.5	1083	6	AAU45753	AaU45753 Human CH2
41	297.2	64.5	1083	8	ABZ24017	ABZ24017 Antibody
42	297.2	64.5	1413	3	AAU63531	AaU63531 DNA encod
43	297.2	64.5	1413	6	AAU45752	AaU45752 Human C2B
44	297.2	64.5	1413	8	ABZ24016	ABZ24016 Antibody
45	297.2	64.5	9208	2	AAU65629	AaU65629 Vector co

ALIGNMENTS

RESULT 1	AAU85150	standard, cDNA, 461 BP.
ID	AAU85150	
XX	AAU85150:	
AC	25-MAR-2003 (revised)	
DT	04-JUN-1998 (first entry)	
XX	Murine monoclonal anti-idiotypic antibody 11D10 VH cDNA.	
XX	Monoclonal anti-idiotypic antibody; mucin;	
KW	human milk fat globule; HMF; tumour; breast cancer; vaccine; ss.	
XX	Mus musculus.	
OS	Key	Location/Qualifiers
XX	FT sig_peptide	1..57
FT	FT mat_peptide	58..461
FT	FT	/*tag= b
XX	W09722699-A2.	
XX	26-JUN-1997.	
XX	19-DEC-1996.	96WO-US020757.
XX	20-DEC-1995.	95US-00575762.
PR	26-JAN-1996.	96US-00591965.
PR	13-DEC-1996.	96US-00766350.
XX	(KENT) UNIV KENTUCKY.	
PA	Chatterjee M, Foon KA, Chatterjee SK,	
XX	WPI: 1997-341690/31.	
DR	P-PSDB; AAU27120.	
XX	Monoclonal anti-idiotypic antibody 11D10 - elicits immune response against	
PT	human milk fat globule disease associated tumours, especially breast	
PT	cancer.	
XX	Claim 12; Page 94; 130pp; English.	

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 13:39:34 ; Search time 2427.45 Seconds
(without alignments)
8980.833 Million cell updates/sec

Title: US-08-836-455-3

Perfect score: 461 ATGGAATGACGCTGGCTTT.....CTGCTCCCTGGAAGCTTGCG 461

Sequence: 1 ATGGAATGACGCTGGCTTT.....CTGCTCCCTGGAAGCTTGCG 461

Scoring table: IDENTITY NUC
Gapop 10_0, Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank! :
1: gb_ba :
2: gb_hcg :
3: gb_in :
4: gb_om :
5: gb_ov :
6: gb_pac :
7: gb_ph :
8: gb_pl :
9: gb_pr :
10: gb_ro :
11: gb_sra :
12: gb_sy :
13: gb_un :
14: gb_vl :*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	461	6	ARI64506 Sequence
2	461	100.0	461	6	BD085738 Methods o
3	409.4	88.8	411	10	AF124720 Mus muscu
4	355.2	77.0	471	10	AB050080 Mus muscu
5	353.6	76.7	457	10	AY178830 Mus muscu
6	337.8	73.3	1542	10	BC002121 Mus muscu
7	328.2	71.2	483	10	MMU39889 Mus muscu
8	327.2	71.0	409	6	BD092129 Mus muscu
9	325	70.5	1544	10	MUSIGH1H1 Mus muscu
10	324.6	70.4	453	6	ARI09947 Mus muscu
11	323	70.1	525	10	MUSIGHALPA Mus muscu
12	323	69.8	540	6	AI3735 variable re
13	322	69.8	458	6	I05821 Sequence 37
14	322	69.8	458	6	I08811 Sequence 12
15	322	69.8	458	6	I09199 Sequence 38
16	322	69.8	458	6	MUSIGHXW Mus muscu
17	322	69.8	459	6	AR431375 Sequence
18	321.6	69.8	450	10	AY178829 Mus muscu
19	320.6	69.5	1553	6	E08434 CDNA encodi

20	320.2	69.5	902	12	XXU49832	U49832 Synthetic s
21	320	69.4	1683	6	E35543	E35543 Transgenic
22	318.6	69.1	473	10	AB050071	AB050071 Mus muscu
23	314.8	68.3	494	6	BD021876	BD021876 Humanized
24	313.4	68.0	451	10	MMUB41HEV	X65773 M. musculus
25	312.6	67.8	534	10	AY621090	AY621090 Mus muscu
26	311.6	67.6	1568	6	E33134	E33134 Humanized a
27	311.6	67.6	1570	6	A22261	A22261 M. musculus
28	311.6	67.6	1570	6	A77138	A77138 Sequence 6
29	311.6	67.5	489	10	MMU39900	U39900 Mus muscu
30	310.8	67.4	1526	10	MMU55622	AJ555622 Mus muscu
31	310.6	67.4	1573	10	BC018280	BC018280 Mus muscu
32	310.2	67.3	1581	6	A78881	A78881 Sequence 1
33	310.2	67.3	1581	10	MMIGHC2AA	X70423 M. musculus
34	310	67.2	1570	6	AR029102	AR029102 Sequence
35	310	67.2	1570	6	AR409372	AR409372 Sequence
36	308.6	66.9	1564	10	BC019489	BC019489 Mus muscu
37	308.2	66.9	588	6	A23165	A23165 Artificial
38	308.2	66.9	588	10	MUSIGVAZ	L02346 Mus muscu
39	308	66.8	490	10	MUSIGCILA	M24785 Mouse anti-
40	308	66.8	1558	10	AF466769	AF466769 Mus muscu
41	307	66.6	484	10	MUSIGH4C11	M54977 Mus muscu
42	306.8	66.6	520	10	MMU416332	AJ416332 Mus muscu
43	306.6	66.5	2154	10	BC018315	BC018315 Mus muscu
44	306.6	66.5	1500	10	MMMANST2	X79907 M. musculus
45	306.2	66.4	1609	10	BC057672	BC057672 Mus muscu

ALIGNMENTS

RESULT 1
LOCUS ARI64506
DEFINITION Sequence 3 from patent US 6274143.
ACCESSION ARI64506
VERSION ARI64506.1 GI:16237556
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 461)
AUTHORS Chatterjee, M. and Foon, K.A.
TITLE Methods of delaying development of HMG-CoA associated tumors using anti-idiotypic antibody 11D10
JOURNAL Patent: US 6274143-A 3 14-AUG-2001;
FEATUSES Location/Qualifiers
source 1..461
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 461; DB 6; Length 461;
Best Local Similarity 100.0%; Pred. No. 2,6e-146;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGGAATGACGCTGGCTTTCTTCTCTCTCTCAATACTACAGGTGCTCCAG 60
1 ATGGAATGACGCTGGCTTTCTTCTCTCTCTCAATACTACAGGTGCTCCAG 60
Db 1 ATGGAATGACGCTGGCTTTCTTCTCTCTCTCAATACTACAGGTGCTCCAG 60
QY 61 GCTTATCTACAGAGCTGCTGGCTGAGCTGAGAGGTCTGGGGCTTCATGGAAGTTC 120
61 GCTTATCTACAGAGCTGCTGGCTGAGCTGAGAGGTCTGGGGCTTCATGGAAGTTC 120
Db 61 GCTTATCTACAGAGCTGCTGGCTGAGCTGAGAGGTCTGGGGCTTCATGGAAGTTC 120
QY 121 TCGAAGCTTCTGGCTACACATTGACCAATTATGCAATGCACTGGTAAGCAGACCT 180
121 TCGAAGCTTCTGGCTACACATTGACCAATTATGCAATGCACTGGTAAGCAGACCT 180
Db 121 TCGAAGCTTCTGGCTACACATTGACCAATTATGCAATGCACTGGTAAGCAGACCT 180
QY 181 GGCAGAGGCTTGGAATGATGGAATATTTTCTGGAATGATGATCTTCAAT 240
181 GGCAGAGGCTTGGAATGATGGAATATTTTCTGGAATGATGATCTTCAAT 240
Db 181 GGCAGAGGCTTGGAATGATGGAATATTTTCTGGAATGATGATCTTCAAT 240
QY 241 CAGAACTTTAAGGCAAGGCTCATGACTGCAAGACATCTCCAGCAGACGCTAATG 300
241 CAGAACTTTAAGGCAAGGCTCATGACTGCAAGACATCTCCAGCAGACGCTAATG 300

Db 241 CAGAACTTTAAGGGGCAAGGCTTCATGACTGACACATCTCCAGACAGCCTACATG 300
Qy 301 CAGATCAGACGCTGACATCTGAAAGACTGCGGCTATTTCTGTGCAAGGGAACCTG 360
Db 301 CAGATCAGACGCTGACATCTGAAAGACTGCGGCTATTTCTGTGCAAGGGAACCTG 360
Qy 361 GAGGGTGTCTGGAATTAATGAGGAGTCAAGAACCTCAGTCAACGGTCTCTGCAAGCAACG 420
Db 361 GAGGGTGTCTGGAATTAATGAGGAGTCAAGAACCTCAGTCAACGGTCTCTGCAAGCAACG 420
Qy 421 ACACCCCAACCGCTCTATCCACTGCTGCTGGAAGCTTGG 461
Db 421 ACACCCCAACCGCTCTATCCACTGCTGCTGGAAGCTTGG 461

RESULT 2
LOCUS BD085738 461 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods of delaying development of HMPG-associated tumors using
ACCESSION BD085738
VERSION BD085738.1 GI:22631348
KEYWORDS JP 2001523269-A/2.
SOURCE unidentified
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 461)
AUTHORS Chatterjee,M. and Foon,K.A.
TITLE Methods of delaying development of HMPG-associated tumors using
JOURNAL anti-idiotypic antibody 11D10.
COMMENT OS The UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
PN JP 2001523269-A/2
PD 20-NOV-2001
PR 12-JUN-1998 JP 199503252
PR 13-JUN-1997 US 60/049540,11-JUN-1998 US 09/096244 PI
MALAYA CHATTERJEE, KENNETH A FOON
PC A61K39/395,A61K39/39//C07K16/42
CC Strandedness: Single;
CC Topology: Linear;
CC Methods of delaying development of HMPG-associated tumors CC
using
CC anti-idiotypic antibody 11D10
FH Key Location/Qualifiers
FT CDS 1..459
FT mat peptide 58.
FT Location/Qualifiers
1..461
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 461; DB 6; Length 461;
Best local Similarity 100.0%; Pred. No. 2.6e-146; Mismatches 0; Indels 0; Gaps 0;
Matches 461; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGAATGACAGTGGGCTCTTCTCTCTCCCTGTCATTAATCACTAGTCCACCTCCAG 60
Db 1 ATGAATGACAGTGGGCTCTTCTCTCTCCCTGTCATTAATCACTAGTCCACCTCCAG 60
Qy 61 GCTTATCTACAGACATCTGGGGCTGAGCTGAGAGTCTGGGGCTCAGTAAGATGTCC 120
Db 61 GCTTATCTACAGACATCTGGGGCTGAGCTGAGAGTCTGGGGCTCAGTAAGATGTCC 120
Qy 121 TCGAAGGCTTCTGGCTACACATGACATTAATGACATGAGTAAAGACACACT 180
Db 121 TCGAAGGCTTCTGGCTACACATGACATTAATGACATGAGTAAAGACACACT 180
Qy 181 GGAAGGCTCTGGAATGGAATATTTTCTGTGAAATGATGATTAATCAAT 240
Db 181 GGAAGGCTCTGGAATGGAATATTTTCTGTGAAATGATGATTAATCAAT 240

Db 181 GGAAGGCTCTGGAATGGAATATTTTCTGTGAAATGATGATTAATCAAT 240
Qy 241 CAGAACTTTAAGGGGCAAGGCTTCATGACTGACACATCTCCAGACAGCCTACATG 300
Db 241 CAGAACTTTAAGGGGCAAGGCTTCATGACTGACACATCTCCAGACAGCCTACATG 300
Qy 301 CAGATCAGACGCTGACATCTGAAAGACTGCGGCTATTTCTGTGCAAGGGAACCTG 360
Db 301 CAGATCAGACGCTGACATCTGAAAGACTGCGGCTATTTCTGTGCAAGGGAACCTG 360
Qy 361 GAGGGTGTCTGGAATTAATGAGGAGTCAAGAACCTCAGTCAACGGTCTCTGCAAGCAACG 420
Db 361 GAGGGTGTCTGGAATTAATGAGGAGTCAAGAACCTCAGTCAACGGTCTCTGCAAGCAACG 420
Qy 421 ACACCCCAACCGCTCTATCCACTGCTGCTGGAAGCTTGG 461
Db 421 ACACCCCAACCGCTCTATCCACTGCTGCTGGAAGCTTGG 461

RESULT 3
LOCUS AF124720 411 bp mRNA linear ROD 22-MAY-2001
DEFINITION Mus musculus immunoglobulin heavy chain mRNA, partial cds.
ACCESSION AF124720
VERSION AF124720.1 GI:14164544
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 411)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus.
TITLE Tripathi,P.K., Qin,H., Bhattacharya-Chatterjee,M., Ceriani,R.L., Foon,K.A. and Chatterjee,S.K.
JOURNAL Construction and characterization of a chimeric fusion protein consisting of an anti-idiotypic antibody mimicking a breast cancer-associated antigen and the cytokine GM-CSF
MEDLINE Hypridoma 18 (2), 193-202 (1999)
PUBMED 99306687
10380019
2 (bases 1 to 411)
REFERENCE Chatterjee,S.K. and Tripathi,P.K.
AUTHORS Direct Submission
JOURNAL Submitted (29-JUN-1999) Internal Medicine, University of Kentucky, 800 Rose Street, Lexington, KY 40536, USA
FEATURES
source Location/Qualifiers
1..411
/organism="Mus musculus"
/mol_type="mRNA"
/strain="BALB/c"
/db_xref="taxon:10090"
1..411
/note="anti-idiotypic antibody 11D10; mimics a breast cancer-associated antigen, human fat globule (HMPG)"
/codon_start=1
/product="immunoglobulin heavy chain"
/protein_id="AAK55119.1"
/db_xref="GI:14164544"
/translation="MKCSWVFLPLISTTGVHSAAYLQSGAEIVRSAGVMSCKAS GTLYSYNHWKQTPGQLEWIGNIPENGGTYVNOFKKASLTLADTSSSTAYMQI SLSLSDSAVYFCARGNMEGALDYNGQTSVVS"

ORIGIN
Query Match 88.8%; Score 409.4; DB 10; Length 411;
Best local Similarity 99.8%; Pred. No. 1.3e-128; Mismatches 1; Indels 0; Gaps 0;
Matches 410; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 ATGAATGACAGTGGGCTCTTCTCTCTCCCTGTCATTAATCACTAGTCCACCTCCAG 60
Db 1 ATGAATGACAGTGGGCTCTTCTCTCTCCCTGTCATTAATCACTAGTCCACCTCCAG 60
Qy 61 GCTTATCTACAGACATCTGGGGCTGAGCTGAGAGTCTGGGGCTCAGTAAGATGTCC 120
Db 61 GCTTATCTACAGACATCTGGGGCTGAGCTGAGAGTCTGGGGCTCAGTAAGATGTCC 120

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2004, 13:29:00 ; Search time 54.9832 Seconds
(without alignments)
1517.360 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 740

Sequence: 1 MGAPAIIGFLLLFPCTRC.....IKADAPVTSIRPPSSKLG 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries.

Database :

UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	642	86.8	127	2	Q925S9
2	596	80.5	130	1	KV5G_MOUSE
3	516	69.7	236	2	Q7TMK3
4	513	69.3	234	2	Q8R062
5	506	68.4	234	2	Q91WF8
6	501	67.7	236	2	Q7TS98
7	492	66.5	233	2	Q91WS9
8	489	66.1	236	2	Q6GMX9
9	475	64.2	236	2	Q6GMX8
10	471	63.6	236	2	Q6GMW1
11	469	63.4	236	2	Q7Z3Y4
12	461	62.3	236	2	Q6PIH7
13	461	62.3	236	2	AAH34141
14	460	62.2	234	2	Q7Z473
15	460	62.2	234	2	Q6PKX4
16	460	62.2	234	2	AAH02112
17	452	61.1	117	1	KV5H_MOUSE
18	450	60.8	234	2	Q8VCF0
19	450	60.8	236	2	Q6GMX0
20	442	59.7	236	2	Q6PRT5
21	442	59.7	236	2	AAH29444
22	433	58.5	214	2	Q9RIAS
23	426	57.6	236	2	AAH34146
24	426	57.6	236	2	AAH34146
25	416.5	56.3	99	2	AAH1068
26	416	56.3	99	2	AAH30813
27	412	55.7	128	1	KV5E_MOUSE
28	408	55.1	111	2	AAH1092
29	403	54.5	103	2	AAH1025
30	394	53.2	129	1	KV1W_HUMAN
31	393.5	53.2	235	2	Q6GMV9

32	391.5	52.9	239	2	Q8K0F8	Q8K0F8 mus musculus
33	390.5	52.8	235	2	Q7TMK0	Q7TMK0 mus musculus
34	389.5	52.6	235	2	Q6GMW0	Q6GMW0 homo sapien
35	389	52.6	108	1	KV5J_MOUSE	P01643 mus musculus
36	384.5	52.0	235	2	Q6PJF2	Q6PJF2 homo sapien
37	384.5	52.0	235	2	AAH16380	AAH16380 homo sapi
38	384	51.9	108	1	KV5J_MOUSE	P01644 mus musculus
39	383	51.8	108	1	KV5O_MOUSE	P01648 mus musculus
40	382.5	51.7	235	2	Q91W12	Q91W12 mus musculus
41	382	51.6	108	1	KV5N_MOUSE	P01646 mus musculus
42	382	51.6	108	1	KV5N_MOUSE	P01647 mus musculus
43	382	51.6	236	2	Q6P5S8	Q6P5S8 homo sapien
44	382	51.6	236	2	AAH62704	AAH62704 homo sapi
45	381	51.5	117	1	KV1I_HUMAN	P01601 homo sapien

ALIGNMENTS

RESULT 1	ID	Q925S9	PRELIMINARY;	PRT;	127 AA.
AC	Q925S9				
DT	01-DEC-2001	(TREMblrel. 19, Created)			
DT	01-DEC-2001	(TREMblrel. 19, Last sequence update)			
DT	01-OCT-2003	(TREMblrel. 25, Last annotation update)			
DE	Immunoglobulin light chain (fragment).				
OS	Mus musculus (mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]	SEQUENCE FROM N.A.			
RP	STRAIN=BALB/c;				
RC	MEDLINE=9306687; PubMed=10380019;				
RA	Tripathi P.K., Qin H., Bhattacharya-Chatterjee M., Ceriani R.L.,				
RA	Poon K.A., Chatterjee S.K.;				
RT	"construction and characterization of a chimeric fusion protein				
RT	consisting of an anti-idiotype antibody mimicking a breast cancer-				
RT	associated antigen and the cytokine GM-CSF."				
RL	Hybridoma 18:193-202(1999).				
DR	EMBL; AF124721; AAK55120.1; -				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003596; Ig_v.				
DR	Pfam; PF00047; Ig_1.				
DR	SMART; SM00406; IgV_1.				
DR	PROSITE; PSS0835; IG_LIKE; 1.				
FT	NON TER				
SQ	SEQUENCE	127 AA; 13794 MW; 13F61BBB981FAS CRC64;			
Query Match		86.8%; Score 642; DB 2; Length 127;			
Best Local Similarity		99.2%; Pred. No. 7.4e-55;			
Matches	126; Conservative	0; Mismatches	1; Indels	0; Gaps	0;
Qy	1	MGAPAIIGFLLLFPCTRCDIOMTOSPSLSASIGORVSLTORASODIGINLHWIQE	60		
Db	1	MRAPAIIGFLLLFPCTRCDIOMTOSPSLSLSLQORVSLTORASODIGINLHWIQE	60		
Qy	61	DGTRKLIYATSSLSGVPKRFSGSRGSDYSLTISLSSEDPVAVYCCIQYASSPYTFG	120		
Db	61	DGTRKLIYATSSLSGVPKRFSGSRGSDYSLTISLSSEDPVAVYCCIQYASSPYTFG	120		
Qy	121	GTYLEIK 127			
Db	121	GTYLEIK 127			
RESULT 2					
ID	KV5G_MOUSE	STANDARD;	PRT;	130 AA.	
AC	P01639; P01640;				
DT	21-JUL-1986 (Rel. 01, Created)				
DT	21-JUL-1986 (Rel. 01, Last sequence update)				

DT 05-JUL-2004 (Rel. 44, last annotation update)
 DE Ig kappa chain V-V region MOPC 41 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=79221900; PubMed=111146;
 RA Seidman U.G., Max E.E., Leder P.;
 RT "A kappa-immunoglobulin gene is formed by site-specific recombination
 RT without further somatic mutation.";
 RL Nature 280:370-375(1979).
 RN [2]
 RP SEQUENCE OF 1-33.
 RX MEDLINE=77148916; PubMed=403522;
 RA Birstein Y., Schechter I.;
 RT "Amino acid sequence of the NH2-terminal extra piece segments of the
 RT precursors of mouse immunoglobulin lambda1-type and kappa-type light
 RT chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 74:716-720(1977).
 RN [3]
 RP SEQUENCE OF 23-130.
 RX MEDLINE=67056897; PubMed=4162931;
 RA Gray W.R., Dreyer W.J., Hood L.;
 RT "Mechanism of antibody synthesis: size differences between mouse kappa
 RT chains.";
 RL Science 155:465-467(1967).
 CC -1- MISCELLANEOUS: This precursor was synthesized in a cell-free
 CC system directed by mRNA isolated from myeloma polyclones.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A93211; KXMSM4.
 DR HSSP; P01594; JLV5.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV_1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Bence-Jones protein; Direct protein sequencing;
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 130 Ig kappa chain V-V region MOPC 41.
 FT DOMAIN 23 45 Framework-1.
 FT DOMAIN 46 56 Complementarity-determining-1.
 FT DOMAIN 57 71 Framework-2.
 FT DOMAIN 72 78 Complementarity-determining-2.
 FT DOMAIN 79 110 Framework-3.
 FT DOMAIN 111 119 Complementarity-determining-3.
 FT DOMAIN 120 129 Framework-4.
 FT DISULFID 45 110 By similarity.
 FT VARIANT 1 2 Missing (in 25% of the molecules).
 FT NON_TER 130 130
 SQ SEQUENCE 130 AA; 14311 MW; 58FE0FE71D5F1BEC CRC64;

Query Match 80.5%; Score 596; DB 1; Length 130;
 Best Local Similarity 92.2%; Pred. No. 2.4e-50;
 Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 MGAPQIIGFLLLPFGTRCDIQMTQSPSSLSASISGQVSLTCRASQDIGINLHWLQOEP 60
 DB 3 MRAPQIFGFLLLPGTRCDIQMTQSPSSLSASISGERVSLTCRASQDIGINLHWLQOEP 62
 QY 61 DGTIRKLIYATSLGSGVPKRPSGSGSDVSLTSSLESDFVAYVYCLQVASSPYTGG 120
 DB 63 DGTIRKLIYATSLGSGVPKRPSGSGSDVSLTSSLESDFVAYVYCLQVASSPYTGG 122
 QY 121 GTKLEIKR 128
 DB 123 GTKLEIKR 130

RESULT 3
 Q7TMK3

ID 07TMK3 PRELIMINARY; PRT; 236 AA.
 AC 07TMK3;
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, last annotation update)
 DE Hypothetical protein.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II;
 RX TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Prange C.,
 RA Boeak S.A., McEwan P.J., McKernan K.J., Matlack J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Hellon E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maitra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CZECH II;
 RX TISSUE=Mammary tumor metastasized to lung. Tumor arose spontaneously;
 RA Strausberg R.;
 RL EMBL; BC055906; AAH55906.1; -;
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; C1-sect; 1.
 DR Pfam; PF00047; IG_1.
 DR SMART; SM00406; IGV_1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 26299 MW; 0DB03488AAA6396F CRC64;

Query Match 69.7%; Score 516; DB 2; Length 236;
 Best Local Similarity 71.3%; Pred. No. 3.3e-42;
 Matches 102; Conservative 12; Mismatches 29; Indels 0; Gaps 0;

QY 1 MGAPQIIGFLLLPFGTRCDIQMTQSPSSLSASISGQVSLTCRASQDIGINLHWLQOEP 60
 DB 3 MRAPQIFGFLLLPGTRCDIQMTQSPSSLSASISGERVSLTCRASQDIGINLHWLQOEP 62
 QY 61 DGTIRKLIYATSLGSGVPKRPSGSGSDVSLTSSLESDFVAYVYCLQVASSPYTGG 120
 DB 63 WSKPKLIYATSLADGVSKRPSGSGSDVSLTSSLESDFVAYVYCLQVASSPYTGG 122
 QY 121 GTKLEIKRADAAPVSIPESSK 143
 DB 123 GTKLEIKRADAAPVSIPESSK 145

RESULT 4
 Q8R062

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2004, 13:29:00 ; Search time 14.5973 Seconds
(without alignments)
955.753 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 740
Sequence: 1 MGAAPQILGFLILFPQTRC.....IKRADAAPVYSIRPSSKLG 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 9621673 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	596	80.5	130	1 KVM5M4	Ig kappa chain pre
2	501	67.7	106	2 PL0260	Ig kappa chain V r
3	497	67.2	106	2 PL0259	Ig kappa chain V r
4	496	67.0	234	2 S14317	Ig kappa chain pre
5	478	64.6	129	2 D32513	Ig kappa chain pre
6	459	62.0	106	2 PL0262	Ig kappa chain V r
7	452	61.1	117	1 KVM53B	Ig kappa chain pre
8	447	60.4	234	2 S01320	Ig kappa chain pre
9	445	60.1	108	4 B47271	Ig kappa chain pre
10	443	59.9	128	2 A26406	Ig kappa chain V r
11	439	59.3	127	2 PH1224	Ig kappa chain pre
12	438	59.2	129	2 S40369	Ig kappa chain - h
13	435	58.8	98	2 PH1062	Ig kappa chain V r
14	435	58.8	126	2 A34904	Ig kappa chain V r
15	434	58.6	125	2 S40353	Ig kappa chain V-J
16	434	58.6	130	2 S40368	Ig kappa chain - h
17	433	58.5	129	2 B23986	Ig kappa chain pre
18	431	58.2	122	2 A29380	Ig kappa chain pre
19	429	58.0	141	2 A49134	Ig kappa chain V-I
20	428.5	57.9	230	2 S33161	Ig kappa chain - s
21	428	57.8	129	2 S40317	Ig kappa chain - h
22	426	57.6	127	2 S52447	Ig kappa chain V r
23	425	57.4	132	2 S40334	Ig kappa chain - h
24	424	57.3	115	2 TL0080	Ig kappa chain pre
25	422	57.0	123	2 S40313	Ig kappa chain V r
26	419	56.6	88	2 PL0261	Ig kappa chain V r
27	419	56.6	129	2 S52789	Ig kappa chain V r
28	419	56.6	131	2 S40352	Ig kappa chain V-J
29	418	56.5	125	2 S40349	Ig kappa chain V-J

30	418	56.5	127	2 S40367	Ig kappa chain V-J
31	416	56.2	129	2 S52793	Ig kappa chain V r
32	415	56.1	128	2 S46372	Ig kappa chain var
33	413	55.8	125	2 S40333	Ig kappa chain V-J
34	412	55.7	128	1 KVM5T1	Ig kappa chain pre
35	410	55.4	123	2 S40331	Ig kappa chain - h
36	410	55.4	132	2 S38646	Ig kappa chain V r
37	409	55.3	128	2 PL0101	Ig kappa chain pre
38	407	55.0	101	2 C28840	Ig kappa chain V r
39	407	55.0	101	2 B28840	Ig kappa chain V r
40	405	54.7	125	2 S40316	Ig kappa chain - h
41	405	54.7	126	2 S40335	Ig kappa chain V-J
42	403.5	54.5	135	2 S24320	Ig kappa chain pre
43	402	54.3	124	2 PL0106	Ig kappa chain pre
44	400.5	54.1	125	2 S40315	Ig kappa chain - h
45	400	54.1	129	2 S52792	Ig kappa chain V r

ALIGNMENTS

RESULT 1

Ig kappa chain precursor V region (MOPC 41) - mouse
N/Contains: Ig kappa chain precursor V region VK41

C/Species: Mus musculus (house mouse)

C/Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #ext change 09-Jul-2004

C/Accession: A93211; B93211; A93815; A94239; A01922; A01923

R/Seidman, J.G.; Max, R.E.; Leder, P.

A/Title: A kappa-immunoglobulin gene is formed by site-specific recombination without f

A/Reference number: A93211; M01D:79221900; E01D:111146

A/Accession: A93211

A/Molecule type: DNA

A/Residues: 1-130 <PC41>

A/Cross-references: UNIPROT:P01639

A/Accession: B93211

A/Molecule type: DNA

A/Residues: 1-117 <VK41>

A/Cross-references: GB:J00804; GB:J00565; NID:952127; PIDN:CA24186.1; PID:9575660

A/Note: the sequences were determined from the differentiated gene MOPC 41 and the germ

Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977

A/Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursor

A/Reference number: A93815; M01D:77148916; E01D:403522

A/Accession: A93815

A/Molecule type: protein

A/Residues: 1-33 <BUR>

A/Note: Met-3 is apparently used as an alternative initiator in 25% of the chains

R/Gray, W.R.; Dreyer, W.J.; Hood, L.

A/Title: Mechanism of antibody synthesis: size differences between mouse kappa chains.

A/Reference number: A94239; M01D:67056897; E01D:416231

A/Accession: A94239

A/Molecule type: protein

A/Residues: 23-49, 'B', '51-53', 'USB', '57-58', 'ZZ', '61-62', 'BZ', '65-76', 'B', '78-108', '110-130' <GRA>

A/Experimental source: Bence Jones protein MOPC 41

C/Genetics:

A/Intons: 19/1

C/Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa)

C/Superfamily: Immunoglobulin V region; immunoglobulin homology

C/Keywords: alternative initiators; heterotrimer; immunoglobulin

F/1-22/Domain: signal sequence #status experimental <SIG1>

F/3-22/Domain: signal sequence #status experimental <SIG2>

F/23-110/Product: Ig kappa chain V region (MOPC 41) #status experimental <M41>

F/28-112/Domain: immunoglobulin homology <IMM>

F/45-110/Disulfide bonds: #status predicted

Query Match 80.5%; Score 596; DB 1; Length 130;
Best Local Similarity 92.2%; Pred. No. 1.5e-42;
Matches 118; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 KGAPOIGFLLLLPGTRCDIQMOSPSLSASIGQRSLTCRASODI GINLHMLQCEP 60
Db 3 MRAPQIGFLLLLQGTRCDIQMOSPSLSASIGQRSLTCRASODIGSSLNLMLQCEP 62
QY 61 DGTIRLLLYAASSLSGVPKPKPSGSRSGSDYSLTISLESEDFVAYCYCLOVASSEPTFGG 120
Db 63 DGTIRLLLYAASSLSGVPKPKPSGSRSGSDYSLTISLESEDFVAYCYCLOVASSEPTFGG 122
QY 121 GTKLEIKR 128
Db 123 GTKLEIKR 130

RESULT 2

IG kappa chain V region (anti-DNA, DP7VK) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 C/Accession: P00260
 R/Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, J.
 J. Exp. Med. 171, 265-297, 1990
 A/Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A/Reference number: P00231; PMID:90111618; PMID:2104919
 A/Accession: P00260
 A/Molecule type: mRNA
 A/Residues: 1-106 <SHL>
 C/Superfamily: Immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F/1-23/Region: framework 1
 F/16-90/Domain: immunoglobulin homology <IMM>
 F/24-34/Region: complementarity-determining 1
 F/35-49/Region: framework 2
 F/50-56/Region: complementarity-determining 2
 F/57-88/Region: framework 3
 F/89-97/Region: complementarity-determining 3
 F/98-106/Region: framework 4

Query Match	67.7%	Score 501;	DB 2;	Length 106;
Best Local Similarity	63.4%	Score 483;	DB 2;	Length 106;

Matches	99; Conservative	4; Mismatches	3; Indels	0; Gaps	0
2000 Local Similarity	93.48;				
	Freq. NO. 8; 96-35;				

QY 21 DIQMTGSPSSLSASLGGORVSLTCRASODIGINLHMLQOEPPDGTIKRLLYATSSLSGGVPK 8
|||||
Dd 1 DIQMTGSPSSLSASLGGORVSLTCRASODIGSSINMLQOEPPDGTIKRLLYATSSLSLDSGVPK 6
|||||

QY		81	RFGSRSGSDYLTISSLESEDVAYCYCLOVASSPYTFGGTKL EI	126
Dp		61	RFGSRSGDYLTISSLESEDFVDYYCLQVASSPMTFFGGTKL EI	106

RESULT 3

Ig kappa chain V region (anti-DNA, DPLVK) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 21-Jan-2000
 C:Accession: PLO259
 R:Shlomchik, M.; Maccell, M.; Shan, H.; Radic, M.Z.; Piletsky, D.; Marshak-Rothstein, J.
 J Exp. Med. 171, 265-287, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A:Reference number: PLO231; PMID:9011618; PMID:2104919
 A:Accession: PLO259

C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Subfamily: IgA1-100 (cna)
C/Keywords: heterotrimeric; immunoglobulin
F/1-23/Region: framework 1
F/16-90/Domain: immunoglobulin homology <IM>
F/24-34/Region: complementarity-determining 1
F/35-49/Region: framework 2
F/50-56/Region: complementarity-determining 1
F/57-88/Region: complementarity-determining 2
F/89-97/Region: complementarity-determining 3
F/98-106/Region: framework 4

Query Match 67.2%; Score 497; DB 2; Length 106;
Best Local Similarity 92.5%; Pred. No. 1.9e-34;
Matches 98; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Seq

21 DIQMTOSESSLSASLGQRVSLTCRASODIGINLHWLQQEEDGTIKRLIYATSSLGSGVPK
80 ||||| :||||| :|||||
1 DIQMTOSESSLSASLGGERVSLTCTCASQDIGRSLNWLQQEEDGTIRLLIYAASSLDGSVPK
60 ||||| :||||| :|||||

```

81 RREGSRSSDYLTLTSSLESEDFVAYYCQYASSPYTFGGTKLEI 126
|||||
61 RREGSRSSDYLTLTSSLESEDFVYDYCYQYATSPMTFGGTKLEI 106
|||||

```

RESULT

```

g kappa chain precursor (15C5) - mouse
;Species: Mus musculus (house mouse)
;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
;Accession: S14237
;Vandamme, A.M.; Bulens, F.; Bernat, H.; Nellès, L.; Lijnen, R.H.; Collen, D.
;Title: Construction and characterization of a recombinant murine monoclonal antibody d
ur. J. Biochem. 192, 767-775, 1990
;Reference number: S14236; MUID:91006173; PMID:2209622
;Accession: S14237
;Molecule type: mRNA
;Residues: 1-234 <VAN>
;Cross-references: EMBL:X56394; NID:G51622; PIN:CA39805.1; PID:G51623
;Superfamily: Immunoglobulin V region; immunoglobulin homology
;Keywords: heterotrimer; immunoglobulin
;36-110/Domain: Immunoglobulin homology <IMM>

```

Query Match	Score	DB 2;	Length
67.0%;	496;	DB 2;	234;
Best Local Similarity	68.5%;	Prod No	10 34

Matches 98; Conservative 15; Mismatches 30; Indels 0; Gaps 0;

1 MGAPAOILGFLILLFPGTRCDIQTOSPSLSASLGQVSLTCRASQDIGINLHWLQOE 60
1 MRTPAQFLGIILLWTFPGIKCDIKMTQSPSSMYASLGERVTVCASQDINSYLSWIQKP 60

[illegible]

```

121  GTKLEIKRADAPTVSIFPPSSK  143
      |||||
121  GTKLEIKRADAPTVSIFPPSSK  143

```

RESULT 5

kappa chain precursor V region (BXWL6) - mouse
 Species: Mus musculus (house mouse)
 Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
 Accession: D32513
 Collier, R.; Strömal, R.; Baldeiras, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
 Miller, R.; Invert, E.; 852-860, 1988
 Title: Immunoglobulin kappa light chain variable region gene complex organization and
 Reference number: A34689; MUID:88331394; PMID:1133286

Molecular type: DNA
 Residues: 1-129 <KOP>
 Cross-references: GB:M20832, NID:g196941, PIDs:AAA38045.1; PID:g19694243
 Superfamily: Immunoglobulin V region; immunoglobulin homology
 Keywords: heterotrimer; immunoglobulin
 38-112/Domain: immunoglobulin homology <IMM>

Query Match	Score	DB 2	Length
64.6%	478	2	129
76.8%	478	2	129

Local similarity 10.0%; Fied. NO. 8.7e-33;
Matches 96; Conservative 6; Mismatches 23; Indels 0; Gaps 0;

3 ARAQIGLLLLFPGTRCDIQMTQSSLSASLGQVSLTCRASQDIGINLHWLQEPDG 62

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: December 6, 2004, 13:34:19 ; Search time 185.386 Seconds

(without alignments)
278.934 Million cell updates/sec

Title: US-08-836-455-2

Sequence: 1 MGAPAIQLFLFLIPGTRC.....IKRADAPVYSIRPSSKLG 145

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/prodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/prodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/prodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/prodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/prodata/1/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/prodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/prodata/1/pubpaa/US10_PUBCOMB.pep:*
- 17: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/prodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	740	100.0	145	9 US-09-861-294-2	Sequence 2, Appl1
2	740	100.0	145	14 US-10-367-506-2	Sequence 2, Appl1
3	626	84.6	144	16 US-10-642-120-4	Sequence 4, Appl1
4	626	84.6	144	16 US-10-642-060-4	Sequence 4, Appl1
5	626	84.6	144	16 US-10-642-122-4	Sequence 4, Appl1
6	626	84.6	144	16 US-10-642-124-4	Sequence 4, Appl1
7	626	84.6	144	16 US-10-621-269-4	Sequence 4, Appl1
8	626	84.6	144	16 US-10-620-850-4	Sequence 4, Appl1
9	626	84.6	144	17 US-10-642-118-4	Sequence 4, Appl1
10	626	84.6	144	17 US-10-642-117-4	Sequence 4, Appl1
11	626	84.6	144	17 US-10-642-119-4	Sequence 4, Appl1
12	626	84.6	144	17 US-10-642-099-4	Sequence 4, Appl1
13	601	81.2	130	8 US-08-779-784-35	Sequence 35, Appl1

14	601	81.2	130	14	US-10-010-729-71	Sequence 71, Appl1
15	541	73.1	130	14	US-10-268-883-11	Sequence 11, Appl1
16	518	70.0	129	8	US-08-973-518-2	Sequence 2, Appl1
17	518	70.0	129	9	US-09-007-093-2	Sequence 2, Appl1
18	518	70.0	129	14	US-10-428-754-2	Sequence 2, Appl1
19	510	68.9	108	14	US-10-010-729-45	Sequence 45, Appl1
20	507	68.5	108	9	US-09-887-853-6	Sequence 6, Appl1
21	506	68.4	108	9	US-09-924-099-1	Sequence 1, Appl1
22	505	68.2	252	15	US-10-239-656-55	Sequence 55, Appl1
23	505	68.2	499	15	US-10-239-656-73	Sequence 73, Appl1
24	503	68.0	108	16	US-10-307-276B-4	Sequence 4, Appl1
25	503	68.0	108	16	US-10-803-622-267	Sequence 267, App
26	503	68.0	108	15	US-10-803-653-267	Sequence 48, Appl1
27	502	67.8	236	16	US-10-038-591-48	Sequence 48, Appl1
28	502	67.8	236	17	US-10-775-444A-48	Sequence 48, Appl1
29	502	67.8	237	9	US-09-924-099-9	Sequence 9, Appl1
30	502	67.8	243	9	US-09-924-099-10	Sequence 10, Appl1
31	501	67.7	257	15	US-10-239-656-67	Sequence 67, Appl1
32	501	67.7	234	16	US-10-684-109-97	Sequence 97, Appl1
33	496	67.0	109	9	US-09-943-906-74	Sequence 74, Appl1
34	496	67.0	109	14	US-10-435-602-74	Sequence 74, Appl1
35	494	66.8	236	15	US-10-038-591-52	Sequence 52, Appl1
36	494	66.8	236	17	US-10-775-444A-52	Sequence 52, Appl1
37	493	66.6	234	16	US-10-684-109-115	Sequence 115, App
38	488	65.9	234	16	US-10-684-109-91	Sequence 91, Appl1
39	488	65.9	234	16	US-10-684-109-109	Sequence 109, App
40	486	65.7	234	16	US-10-684-109-103	Sequence 103, App
41	479	64.7	148	14	US-10-222-026A-25	Sequence 25, Appl1
42	479	64.7	287	14	US-10-222-026A-37	Sequence 37, Appl1
43	475	64.2	236	15	US-10-038-591-51	Sequence 51, Appl1
44	475	64.2	236	17	US-10-775-444A-51	Sequence 51, Appl1
45	474	64.1	234	14	US-10-292-088-24	Sequence 24, Appl1

ALIGNMENTS

RESULT 1
US-09-861-294-2 ; Sequence 2, Application US/09861294
; Patent No. US20020098190A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-09-861-294-2

Query Match 100.0%; Score 740; DB 9; Length 145;
Best local Similarity 100.0%; Pred. No. 5.8e-55;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAIQLFLFLIPGTRCDIOMTSPSSLSAGLQGVSLTCRASQDIGINLHWLQGP 60
DB 1 MGAPAIQLFLFLIPGTRCDIOMTSPSSLSAGLQGVSLTCRASQDIGINLHWLQGP 60
QY 61 DGIIRKLIVATSSLSGSGVRKFRPSGSGSDYSLTISLSSEDFVAYICQYASPTTFGG 120

```
Db      61 DGTIKRLIYATSSLSGSGVPRKFRFSGSRGSDYSLTISLESDEDFVAYYCLQYASSPYTFGG 120
QY      121 GTKLEIKRADAAPTVSIFFPSSKLG 145
Db      121 GTKLEIKRADAAPTVSIFFPSSKLG 145
```

RESULT 2

```
US-10-367-506-2
; Sequence 2, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHARTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; FILE OF INVENTION: TUMORS BEARING HMF AND CEA ANTIGENS
; FILE REFERENCE: 304142000620
; CURRENT APPLICATION NUMBER: US/10/367,506
; PRIOR FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/861,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 145
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)...(20)
US-10-367-506-2
```

```
Query Match      100.0%; Score 740; DB 14; Length 145;
Best Local Similarity 100.0%; Pred. No. 5.8e-55;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 MGAPOIILGFLLLFPGRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHMLQGP 60
Db      1 MGAPOIILGFLLLFPGRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHMLQGP 60
QY      61 DGTIKRLIYATSSLSGSGVPRKFRFSGSRGSDYSLTISLESDEDFVAYYCLQYASSPYTFGG 120
Db      61 DGTIKRLIYATSSLSGSGVPRKFRFSGSRGSDYSLTISLESDEDFVAYYCLQYASSPYTFGG 120
QY      121 GTKLEIKRADAAPTVSIFFPSSKLG 145
Db      121 GTKLEIKRADAAPTVSIFFPSSKLG 145
```

RESULT 3

```
US-10-642-120-4
; Sequence 4, Application US/10642120
; Publication No. US20040131610A1
; GENERAL INFORMATION:
; APPLICANT: Thorpe, Philip E.
; APPLICANT: Soares, M. Melina
; APPLICANT: Ran, Sophia
; TITLE OF INVENTION: Methods for Treating Viral Infections Using Antibodies to
; FILE REFERENCE: 4001.002900
; CURRENT APPLICATION NUMBER: US/10/642,120
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/621,269
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
```

```
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-120-4
```

```
Query Match      84.6%; Score 626; DB 16; Length 144;
Best Local Similarity 90.6%; Pred. No. 2.5e-45;
Matches 125; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
```

```
QY      1 MGAPOIILGFLLLFPGRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHMLQGP 60
Db      3 MGAPOIILGFLLLFPGRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHMLQGP 62
QY      61 DGTIKRLIYATSSLSGSGVPRKFRFSGSRGSDYSLTISLESDEDFVAYYCLQYASSPYTFGG 120
Db      63 DGTIKRLIYATSSLSGSGVPRKFRFSGSRGSDYSLTISLESDEDFVAYYCLQYASSPYTFGA 122
QY      121 GTKLEIKRADAAPTVSIFF 138
Db      123 GTKLEIKRADAAPTVIF 140
```

RESULT 4

```
US-10-642-060-4
; Sequence 4, Application US/10642060
; Publication No. US20040131621A1
; GENERAL INFORMATION:
; APPLICANT: Thorpe, Philip E.
; APPLICANT: Soares, M. Melina
; APPLICANT: Ran, Sophia
; TITLE OF INVENTION: Combinations and Kits for Treating Viral Infections Using Antibod
; FILE REFERENCE: 4001.002982
; CURRENT APPLICATION NUMBER: US/10/642,060
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: US 10/621,269
; PRIOR FILING DATE: 2003-07-15
; PRIOR APPLICATION NUMBER: 60/396,263
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-642-060-4
```

```
Query Match      84.6%; Score 626; DB 16; Length 144;
Best Local Similarity 90.6%; Pred. No. 2.5e-45;
Matches 125; Conservative 4; Mismatches 9; Indels 0; Gaps 0;
```

```
QY      1 MGAPOIILGFLLLFPGRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHMLQGP 60
Db      3 MGAPOIILGFLLLFPGRCDIQMTQSPSSLSASLGQVSLTCRASQDIGINLHMLQGP 62
QY      61 DGTIKRLIYATSSLSGSGVPRKFRFSGSRGSDYSLTISLESDEDFVAYYCLQYASSPYTFGG 120
Db      63 DGTIKRLIYATSSLSGSGVPRKFRFSGSRGSDYSLTISLESDEDFVAYYCLQYASSPYTFGA 122
QY      121 GTKLEIKRADAAPTVSIFF 138
Db      123 GTKLEIKRADAAPTVIF 140
```

RESULT 5

```
US-10-642-122-4
; Sequence 4, Application US/10642122
; Publication No. US20040131622A1
; GENERAL INFORMATION:
; APPLICANT: Thorpe, Philip E.
; APPLICANT: Soares, M. Melina
; APPLICANT: Ran, Sophia
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 15:14:29 ; Search time 649.102 Seconds
(without alignments)
3682.388 Million cell updates/sec

Title: US-08-836-455-1

Perfect score: 435
Sequence: 1 ATGGGGGGCCCCCTGCTCAGAT.....CACCATCCAGTAAGCTTGGG 435

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3694831 seqs, 2747406616 residues

Total number of hits satisfying chosen parameters: 7389662

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
13: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq:*
14: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/prodata/1/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/prodata/1/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/prodata/1/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
20: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	435	100.0	435	9	US-09-861-294-1
2	435	100.0	435	15	US-10-567-506-1
3	384.6	88.4	407	9	US-09-924-099-27
4	372.4	85.6	435	17	US-10-642-120-3
5	372.4	85.6	435	17	US-10-642-060-3
6	372.4	85.6	435	17	US-10-642-122-3
7	372.4	85.6	435	17	US-10-642-124-3
8	372.4	85.6	435	17	US-10-621-269-3
9	372.4	85.6	435	17	US-10-620-850-3
10	372.4	85.6	435	18	US-10-642-118-3
11	372.4	85.6	435	18	US-10-642-117-3
12	372.4	85.6	435	18	US-10-642-119-3

13	372.4	85.6	435	18	US-10-642-099-3	Sequence 3, Appl1
14	372	85.5	402	8	US-08-779-784-5	Sequence 5, Appl1
15	372	85.5	402	15	US-10-010-729-5	Sequence 5, Appl1
16	329.6	75.8	390	15	US-10-268-883-10	Sequence 10, Appl1
17	323.4	74.3	387	8	US-08-973-518-1	Sequence 1, Appl1
18	323.4	74.3	387	9	US-09-007-093-1	Sequence 1, Appl1
19	323.4	74.3	387	15	US-10-428-754-1	Sequence 1, Appl1
20	323.2	74.3	351	8	US-08-779-784-17	Sequence 17, Appl1
21	322.6	74.2	351	8	US-08-779-784-16	Sequence 16, Appl1
22	311.2	71.5	324	15	US-10-010-729-46	Sequence 46, Appl1
23	309.4	71.1	729	9	US-09-887-853-5	Sequence 5, Appl1
24	308.4	70.9	729	9	US-09-924-099-20	Sequence 20, Appl1
25	307.4	70.7	711	9	US-09-924-099-11	Sequence 19, Appl1
26	306.4	70.4	324	9	US-09-924-099-11	Sequence 11, Appl1
27	301.4	69.3	771	16	US-10-239-656-54	Sequence 54, Appl1
28	301.4	69.3	1457	16	US-10-239-656-66	Sequence 66, Appl1
29	301.4	69.3	1457	16	US-10-239-656-72	Sequence 72, Appl1
30	292	67.1	324	17	US-10-307-276B-2	Sequence 2, Appl1
31	284.4	65.4	456	15	US-10-222-026A-26	Sequence 26, Appl1
32	282.4	64.9	867	15	US-10-222-026A-38	Sequence 38, Appl1
33	268.4	61.7	453	16	US-10-395-894-24	Sequence 24, Appl1
34	268.4	61.7	453	17	US-10-695-667-24	Sequence 24, Appl1
35	268.4	61.7	702	17	US-10-684-109-89	Sequence 89, Appl1
36	268.4	61.7	702	17	US-10-684-109-90	Sequence 90, Appl1
37	268.4	61.7	702	17	US-10-684-109-95	Sequence 95, Appl1
38	268.4	61.7	702	17	US-10-684-109-96	Sequence 96, Appl1
39	268.4	61.7	702	17	US-10-684-109-107	Sequence 107, Appl1
40	268.4	61.7	702	17	US-10-684-109-108	Sequence 108, Appl1
41	268.4	61.7	702	17	US-10-684-109-113	Sequence 113, Appl1
42	268.4	61.7	702	17	US-10-684-109-114	Sequence 114, Appl1
43	268.4	61.7	6082	16	US-10-395-894-10	Sequence 10, Appl1
44	268.4	61.7	6082	17	US-10-695-667-10	Sequence 10, Appl1
45	267.6	61.5	447	9	US-09-797-481-1	Sequence 1, Appl1

ALIGNMENTS

RESULT 1

US-09-861-294-1

Sequence 1, Application US/09861294

Patent No. US20020098190A1

GENERAL INFORMATION:

APPLICANT: Malaya CHARTERJEE

APPLICANT: Kenneth A. FOON

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING TUMORS BEARING HMG AND CEA ANTIGENS

FILE REFERENCE: 30414200620

CURRENT APPLICATION NUMBER: US/09/861,294

CURRENT FILING DATE: 2001-05-17

PRIOR APPLICATION NUMBER: 60/049,540

PRIOR FILING DATE: 1997-06-13

PRIOR APPLICATION NUMBER: 09/096,244

PRIOR FILING DATE: 1998-06-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 1

LENGTH: 435

TYPE: DNA

ORGANISM: Mus musculus

FEATURE:

NAME/KEY: CDS

LOCATION: (1)...(435)

NAME/KEY: (1)...(435)

NAME/KEY: s1g_peptide

LOCATION: (1)...(60)

NAME/KEY: mat_peptide

LOCATION: (61)...(435)

Query Match 100.0%; Score 435; DB 9; Length 435;
Best Local Similarity 100.0%; Pred. No. 6.7e-134;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ATGGGGGGCCCTGCTCAGATTTCTTGGGTTCTTGCTCTTGTTTCCAGAGTACAGATGT	60
Db	1	ATGGGGGGCCCTGCTCAGATTTCTTGGGTTCTTGCTCTTGTTTCCAGAGTACAGATGT	60
QY	61	GACATCCAGATGAGCCCAAGTCTCCATCCTCTTATCTGAGCTCTCTGGGACAAAGAGTCA	120
Db	61	GACATCCAGATGAGCCCAAGTCTCCATCCTCTTATCTGAGCTCTCTGGGACAAAGAGTCA	120
QY	121	CTCACTTGTGGGGCAAGTCAAGACATTGGATTAACTTACATTGGCTTCAGCAGGAACA	180
Db	121	CTCACTTGTGGGGCAAGTCAAGACATTGGATTAACTTACATTGGCTTCAGCAGGAACA	180
QY	181	GATGAACTATTAAAGCCCTGATCTTACAGCCACAATCCAGTTAGTTGTTGGTGTCCCAAA	240
Db	181	GATGAACTATTAAAGCCCTGATCTTACAGCCACAATCCAGTTAGTTGTTGGTGTCCCAAA	240
QY	241	AGTTTCAGTGGCAGTAGAGTCTGGGTCAGATTATTTCTTCAACATAGAGACCTTGAAGTCT	300
Db	241	AGTTTCAGTGGCAGTAGAGTCTGGGTCAGATTATTTCTTCAACATAGAGACCTTGAAGTCT	300
QY	301	GAAATTTTGTAGCTTATTACTGTCTTACAAATATGCTAAGTTCTCCGTCACAGTTGGAGGG	360
Db	301	GAAATTTTGTAGCTTATTACTGTCTTACAAATATGCTAAGTTCTCCGTCACAGTTGGAGGG	360
QY	361	GGGACCAAGCTGGAATTAATAACGGGCTGATGTCGACCAACGTATCCATTTTCCCAACA	420
Db	361	GGGACCAAGCTGGAATTAATAACGGGCTGATGTCGACCAACGTATCCATTTTCCCAACA	420
QY	421	TCCAGTAAAGTTGGG 435	
Db	421	TCCAGTAAAGTTGGG 435	

```

RESULT 2
US-10-367-506-1
; Sequence 1, Application US/10367506
; Publication No. US20030152575A1
; GENERAL INFORMATION:
; APPLICANT: Malaya CHATTERJEE
; APPLICANT: Kenneth A. FOON
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: TUMORS BEARING HMGs AND CEA ANTIGENS
; FILE REFERENCE: 304142000630
; CURRENT APPLICATION NUMBER: US/10/367,506
; CURRENT FILING DATE: 2003-02-13
; PRIOR APPLICATION NUMBER: US/09/661,294
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/049,540
; PRIOR FILING DATE: 1997-06-13
; PRIOR APPLICATION NUMBER: 09/096,244
; PRIOR FILING DATE: 1998-06-11
; NUMBER OF SEQ. ID NOS: 39
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 435
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(435)
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: (1)...(60)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (61)...(435)
; US-10-367-506-1

```

Query Match 100.0%; Score 435; DB 15; Length 435;
Best Local Similarity 100.0%; Pred. No. 6.7e-134;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ATGGGGCCCCCTGCTGAGATTCCTTGGGATCTTGTTGCTTGTTCCAGATCCAGATGT 60

Qy 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGATCAGT 120

Db 61 GACATCCAGATGACCCAGTCTCCATCTCTTATCTGCTCTCTGGGACAAAGATCAGT 120

Qy 121 CTCATCTTGCGGGCAAGTACAGGACATGGTATTAATTACATTTGACTTCAGCAGAAACA 180

Db 121 CTCATCTTGCGGGCAAGTACAGGACATGGTATTAATTACATTTGACTTCAGCAGAAACA 180

Qy 181 GATGGAACTTTAAAGGCTGATCTTACGCCACATCCAGTTTAAAGTTCTGTTGCCCAA 240

Db 181 GATGGAACTTTAAAGGCTGATCTTACGCCACATCCAGTTTAAAGTTCTGTTGCCCAA 240

Qy 241 AGGTCAGTGGCAGTAGATCTGGGTCAGATTATCTCCACATCCACAGCTTGAGTCT 300

Db 241 AGGTCAGTGGCAGTAGATCTGGGTCAGATTATCTCCACATCCACAGCTTGAGTCT 300

Qy 301 GAAGATTTGTAGCTTACTTACTGTCTTAACAATATGCTAGTATCTCCGTCACAGTTCCAGAGG 360

Db 301 GAAGATTTGTAGCTTACTTACTGTCTTAACAATATGCTAGTATCTCCGTCACAGTTCCAGAGG 360

Qy 361 GGGACCAAGCTGGAATTAATAAGGGCTGATGCTGACCAACTGTATTCATCTTCCACCA 420

Db 361 GGGACCAAGCTGGAATTAATAAGGGCTGATGCTGACCAACTGTATTCATCTTCCACCA 420

Qy 421 TCCAGTAACTTGGG 435

Db 421 TCCAGTAACTTGGG 435

```

RESULT 3
US-09-924-099-27
: Sequence 27, Application US/09924099
: Patent No. US20020128450A1
: GENERAL INFORMATION:
: APPLICANT: NISHIDA, Yoshihiro
: APPLICANT: OKURA, Takamori
: APPLICANT: TANIMOTO, Tadao
: APPLICANT: KURIMOTO, Masashi
: TITLE OF INVENTION: PEPTIDE
: FILE REFERENCE:
: CURRENT APPLICATION NUMBER: US/09/924,099
: CURRENT FILING DATE: 2001-08-08
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/338,511
: PRIOR FILING DATE: EARLIER FILING DATE: 1999-06-23
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 289,044/98
: PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-12
: PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: JP 365,023/98
: NUMBER OF SEQ ID NOS: 33
: SEQ ID NO 27
: LENGTH: 407
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(407)
: NAME/KEY: sig peptide
: LOCATION: (1)...(60)
: US-09-924-099-27

```

Query Match	88.4%	Score 384.6;	DB 9;	Length 407;
Best Local Similarity	96.6%	Pred. No. 3,7e-117;		
Matches 393;	Conservative 0;	Mismatches 14;	Indels 0;	Gaps 0;
QY	1	ATGGGGGCCCCCTGCTCAGATCTTGAGTTCTTGTGCTCTGTTCCAGGTCCGAGAT	60	
Db	1	ATGAGAGGCCCTGCTCAGATTTTGGCTTCTTCTCTGTTCCAGGTACCGAGAT	60	
QY	61	GACATCCAGATGACCCAGTCTCCATCTCTTAATGCTCTCTGGGCAAAAGTCAGT	120	

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2004, 13:29:00 ; Search time 15.5705 Seconds
(Without alignments)
617.586 Million cell updates/sec

Title: US-08-836-455-2

Sequence: 1 MGAPAOILGFLLLFPGRTRC.....IKRADAAPVTSIRPPSSKLG 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	740	100.0	145	3	US-09-096-244-2
2	518	70.0	129	3	US-08-943-136-2
3	518	70.0	129	3	US-08-973-518-2
4	507	68.5	243	1	US-08-133-804-6
5	507	68.5	243	1	US-08-461-838-6
6	507	68.5	243	2	US-08-461-886-6
7	507	68.5	243	2	US-08-356-786-4
8	503	68.0	534	2	US-08-356-786-4
9	486	67.0	109	2	US-08-713-939A-74
10	486	67.0	109	3	US-09-036-579-74
11	486	67.0	109	3	US-09-550-374-74
12	496	67.0	109	4	US-09-943-906-74
13	492	66.5	107	3	US-08-483-749A-26
14	483	65.3	138	2	US-08-480-434-63
15	483	65.3	138	2	US-08-053-451B-63
16	479	64.7	128	4	US-09-318-786-25
17	479	64.7	128	4	US-09-318-786-25
18	479	64.7	287	4	US-09-318-786-37
19	471	63.6	112	4	US-09-527-218B-1
20	471	63.6	142	3	US-08-579-940-2
21	471	63.6	142	3	US-08-838-692-4
22	468	63.2	107	2	US-08-888-366-14
23	468	63.2	107	2	US-08-888-366-20
24	463	62.6	107	2	US-08-888-366-26
25	461	62.3	131	1	US-08-236-520-2
26	461	62.3	131	5	PCT-US95-05262-2
27	455	61.5	109	1	US-07-942-245-1

28	455	61.5	127	4	US-09-647-468-183	Sequence 183, App
29	454	61.4	127	4	US-09-647-468-182	Sequence 182, App
30	451	60.9	127	4	US-09-647-468-180	Sequence 180, App
31	447	60.4	127	4	US-09-647-468-179	Sequence 179, App
32	446	60.3	129	4	US-09-647-468-161	Sequence 161, App
33	445	60.1	127	4	US-09-647-468-181	Sequence 181, App
34	445	60.1	234	4	US-09-740-002-24	Sequence 24, App
35	444	60.0	127	1	US-08-458-516-5	Sequence 5, App
36	442	59.7	109	2	US-08-713-939A-73	Sequence 73, App
37	442	59.7	109	3	US-09-036-579-73	Sequence 73, App
38	442	59.7	109	3	US-09-550-374-73	Sequence 73, App
39	442	59.7	109	4	US-09-943-906-73	Sequence 73, App
40	442	59.7	215	2	US-08-737-129A-8	Sequence 8, App
41	441	59.6	127	1	US-08-137-117D-29	Sequence 29, App
42	441	59.6	127	2	US-08-436-717-29	Sequence 29, App
43	441	59.6	235	4	US-08-812-586-16	Sequence 16, App
44	441	59.6	235	4	US-09-535-832A-17	Sequence 17, App
45	439	59.3	127	4	US-09-647-468-162	Sequence 162, App

ALIGNMENTS

RESULT 1
US-09-096-244-2
Sequence 2, Application US/09096244
Patent No. 6274143
GENERAL INFORMATION:
APPLICANT: Chatterjee, Malaya
TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
NUMBER OF INVENTIONS: 4
CORRESPONDENCE ADDRESSES:
ADDRESSER: MORRISON & FORSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/096,244
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Polizzi, Catherine M.
REGISTRATION NUMBER: 40,130
REFERENCE/DOCKET NUMBER: 30414-20006.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-096-244-2

Query Match 100.0% ; Score 740 ; DB 3 ; Length 145 ;
Best Local Similarity 100.0% ; Pred. No. 5.6e-63 ;
Matches 145 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
QY 1 MGAPAOILGFLLLFPGRTRCDIQMTSPSSLSASLQGRVSLTCRASQDIGINLHWLQOE 60
DB 1 MGAPAOILGFLLLFPGRTRCDIQMTSPSSLSASLQGRVSLTCRASQDIGINLHWLQOE 60

QY 61 DGTIKRLIYATSSLSGSGVPRFSGSSGSDYSLTSSLESBDFAVAYCYCLQVASSPYTGG 120

Dd 61 DGTIKRLIYATSSLSGSGVPRFSGSSGSDYSLTSSLESBDFAVAYCYCLQVASSPYTGG 120

OY 121 GTKLEIRADAPVSIFFPSSKLG 145

Dd 121 GTKLEIRADAPVSIFFPSSKLG 145

RESULT 2
ITS-08-94

```

US-08-943-136-2
/ Sequence 2, Application US/08943136
/ Patent No. 6231208
/
/ GENERAL INFORMATION:
/ APPLICANT: Amand, Naveen N
/ APPLICANT: Barber, Brian H
/ APPLICANT: Cates, George A
/ APPLICANT: Caterini, Judith E
/ APPLICANT: Klein, Michel H
/ TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
/ TITLE OF INVENTION: ANTIGENS TO SELECTED CELLS OF THE IMMUNE SYSTEM
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Sim & McBurney
/ STREET: 6th Floor, 330 University Avenue
/ CITY: Toronto
/ STATE: Ontario
/ COUNTRY: Canada
/ ZIP: M5G 1R7
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/943,136
/ FILING DATE:
/
/ CLASSIFICATION: 536
/
/ PRIORITY INFORMATION:
/ APPLICATION NUMBER: US 08/483,576
/ FILING DATE: 07-JUNE-1995
/ CLASSIFICATION: 536
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Stewart, Michael I
/ REGISTRATION NUMBER: 24,973
/ REFERENCE/DOCKET NUMBER: 1038-733
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (416) 595-1155
/ TELEFAX: (416) 595-1163
/
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 129 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-08-943-136-2

```

Query Match	70.0%	Score 518;	DB 3;	Length 129;
Best Local Similarity	80.3%	Prod No. 6.2e-42;		
Matches 102; Conservative	7;	Mismatches 19;	Indels 0;	Gaps 0;

[illegible]

RESULT 3
US-08-973-518-2

Query Match	70.0%;	Score 518;	DB 3;	Length 129;
Best Local Similarity	80.3%;	Pred. No. 6, 2e-42;		
Matches 102; Conservative	7;	Mismatches 18;	Indels 0;	Gaps 0;

QY 1KGAPQAIIGFLLILFPGTRCIIOMTQSPSSLSASIGORVSLTCASODIGINLHWLOEP 60
 Db 3MRVPAHVGFLLWPGTRCIDIOMTQSPSSLSASIGORVSLTCASODEISGLHWLOKP 62
 QY 61DGTIRRLIYAASIGVPRKPSGSGSDSLTISLSSEHDFPAAYICLOAYASEPTFFG 120
 Db 63DGTIRRLIYAASITLDSGVPRKPSGSGSDSLTISLSSEHDFADYICLOAYNPILTEGA 122
 QY 121GTKLEIK 127
 Db 123GTKLEIK 129

RESULT 4
 US-08-133-804-6
 Sequence 6, Application US/08133804
 Patent No. 5534254
 GENERAL INFORMATION:
 APPLICANT: Huston, James S.
 APPLICANT: Oppermann, Hermann
 APPLICANT: Houston, U. L.
 APPLICANT: King, David B.
 TITLE OF INVENTION: Biosynthetic Binding Proteins FOR
 TITLE OF INVENTION: Imaging

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 6, 2004, 13:29:00 ; Search time 52.0638 Seconds
(without alignments)
999.078 Million cell updates/sec

Title: US-08-836-455-2

Perfect score: 740

Sequence: 1 MGNAPQILGLFLLLPGRRC.....IKRADAPRVISIPPSKLG 145

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 35872929 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1980s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	740	100.0	145	2	AAW27119 Murine mo
2	740	100.0	145	6	AAO16292 Mouse 11D
3	727	98.2	145	2	AAW87593 Antibody
4	662	89.5	146	1	AAAP30251 Sequence
5	645	87.2	153	8	ADJ57089 3G4-2BVL-
6	633	85.5	135	3	AAV44599 Mouse 11G
7	626	84.6	144	8	ADJ57086 3G4 antib
8	601	81.2	130	6	ADJ26551 Human ant
9	541	73.1	130	6	AAO23070 Murine an
10	527	71.2	129	2	AAW22537 Murine an
11	527	71.2	129	5	AAW20200 Murine 44
12	527	71.2	129	8	ADJ1873 Murine 44
13	518	70.0	129	5	AAW20204 Murine 44
14	510	68.9	108	8	ADJ26702 Mouse ant
15	508	68.6	246	2	AAW39569 Sequence
16	507	68.5	243	2	AAW02280 520C9 ant
17	507	68.5	243	2	AAW53170 520C9 ant
18	507	68.5	243	2	AAW80424 520C9 sFV
19	506	68.4	243	7	ABW00716 520C9 sFV
20	506	68.4	108	3	AAV44587 Mouse ant
21	505	68.2	252	5	AAU72863 PA-14 sIn
22	505	68.2	499	5	AAU72872 JBI0Xp4-1
23	504	68.1	107	2	AAW27121 Murine an
24	503	68.0	108	2	AAW21310 Light cha
25	503	68.0	108	8	ADW00443 Mouse ant

26	503	68.0	144	2	AAW15322 IL-2 chIm
27	503	68.0	146	4	AAW89115 Human pro
28	502	67.8	236	5	ABG77160 GermLine
29	502	67.8	237	3	AAV44595 EacFV#125
30	502	67.8	243	3	AAV44596 EacFV#125
31	502	67.8	257	5	AAU72869 PS-11 sIn
32	501	67.7	237	7	ADW57549 Human Pro
33	501	67.7	237	7	ADW47098 Human Pro
34	501	67.7	237	7	ADW48668 Human Pro
35	497	67.2	144	2	AAW15321 IL-2 chIm
36	496	67.0	109	2	AAW18271 PrP 37 11
37	496	67.0	109	2	AAW85910 PrP 37 11
38	496	67.0	109	4	AAW65862 Anti-PrP
39	496	67.0	109	5	ABP51796 Anti-PrP
40	496	67.0	109	6	ABU58877 Anti-PrP
41	495	66.9	534	2	AAW39571 Sequence
42	494	66.8	236	5	ABG77164 GermLine
43	492	66.5	107	3	AAV90824 520C9 hyb
44	488	65.9	129	6	ABW55313 Amino acI
45	486	65.7	236	8	ADP07905 Human imm

ALIGNMENTS

RESULT 1	AAW27119	standard; protein; 145 AA.
ID	AAW27119	
XX	XX	
AC	AAW27119;	
XX	XX	
DT	25-MAR-2003	(revised)
DT	04-JUN-1998	(first entry)
DE	Murine monoclonal anti-idiotypic antibody 11D10 VL region.	
DE	Monoclonal antibody 11D10; anti-idiotypic antibody; mucin;	
KW	human milk fat globule; HMFg; tumour; breast cancer; vaccine.	
KW	Mus musculus.	
OS	XX	
XX	XX	
FX	Key	Location/Qualifiers
FT	Peptide	1..20
FT	Protein	21..145
FT	Region	/label= Mat_protein
FT	Region	21..43
FT	Region	/label= FRI
FT	Region	/note= "framework region 1"
FT	Region	44..54
FT	Region	/label= CDR1
FT	Region	/note= "complementarity determining region 1"
FT	Region	55..69
FT	Region	/label= FR2
FT	Region	/note= "framework region 2"
FT	Region	70..76
FT	Region	/label= CDR2
FT	Region	/note= "complementarity determining region 2"
FT	Region	77..108
FT	Region	/label= FR3
FT	Region	/note= "framework region 3"
FT	Region	109..117
FT	Region	/label= CDR3
FT	Region	/note= "complementarity determining region 3"
FT	Region	118..127
FT	Region	/label= FR1
FT	Region	/note= "framework region 4"
PN	WO9722699-A2.	
XX	26-JUN-1997.	
PD	19-DEC-1996;	96WO-US020757.
PF		

XX 20-DEC-1995; 95US-00575762.
PR 26-JAN-1996; 96US-00591965.
PR 13-DEC-1996; 96US-00766350.
XX
PA (KENT) UNIV KENTUCKY.
XX
PI Chatterjee M, Foon KA, Chatterjee SK;
XX
DR WPI, 1997-341690/31.
DR N-PSDB; AAT85149.
XX
XX Monoclonal anti-idiotypic antibody 11D10 - elicits immune response against
PT human milk fat globule disease associated tumours, especially breast
PT cancer.
XX
PS Claim 9, Page 94; 130pp; English.
XX

CC This polypeptide sequence comprises the light chain variable region (VL)
CC of monoclonal anti-idiotypic antibody 11D10 produced by hybridoma cell
CC line ATCC 12020. 11D10 was obtained by immunising naive mice with WC-10
CC anti-HMG antibody to obtain an anti-idiotypic response. It elicits an
CC immune response against a specific epitope of a high mol.wt. mucin of
CC human milk fat globule (HMG). It induces an immunological response to
CC HMG in mice, rabbits, monkeys and patients with advanced HMG-associated
CC tumours. Pharmaceutical compositions and vaccines comprising 11D10, 11D10
CC polypeptides and/or 11D10 polynucleotides (see also AAT85149-50) are
CC claimed. Also claimed are diagnostic kits and methods of using 11D10,
CC 11D10 polypeptides and/or 11D10 polynucleotides, including methods of
CC treating HMG-associated tumours. 11D10 is also used in a claimed method
CC of palliating HMG-associated disease and in claimed kits to detect or
CC quantify anti-HMG antibody. (Updated on 25-MAR-2003 to correct PR
CC field.)
XX
SQ Sequence 145 AA;

Query Match 100.0%; Score 740; DB 2; Length 145;
Best Local Similarity 100.0%; Pred. No. 3e-48;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAIIGFLLLPFGTRCDIQMTQSPSSLSASLGQRVSLTCRASODIGINLHMLQOEP 60
DB 1 MGAPAIIGFLLLPFGTRCDIQMTQSPSSLSASLGQRVSLTCRASODIGINLHMLQOEP 60
QY 61 DGTIKRLIYATSSLSGSGVPKRFSGSGSDYSLTISLSIEDPFAVYCLQYASSPYTFGG 120
DB 61 DGTIKRLIYATSSLSGSGVPKRFSGSGSDYSLTISLSIEDPFAVYCLQYASSPYTFGG 120
QY 121 GTKLEIKRADAAPTVSIFFPSSKLG 145
DB 121 GTKLEIKRADAAPTVSIFFPSSKLG 145

RESULT 2
AAOI6292
ID AAOI6292 standard; protein; 145 AA.
XX
AC AAOI6292;
XX
DT 20-MAR-2003 (first entry)
XX
DE Mouse 11D10 antibody light chain variable region.
XX
XX Mouse; murine; vaccine; tumour; human milk fat globules; HMG;
KM carcinoembryonic antigen; CEA; 11D10; 3H1; HMGF-associated tumour;
KM CEA-associated tumour; anti-idiotypic antibody.
XX
OS Mus musculus.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /label=signal_peptide
FT 21..145

/note="Mature murine 11D10 antibody light chain variable
region"

MO200292012-A2.

21-NOV-2002.

17-MAY-2002; 2002WO-US015840.

17-MAY-2001; 2001US-00861294.

(KENT) UNIV KENTUCKY RES FOUND.

Chatterjee M, Foon KA;

WPI; 2003-129216/12.
N-PSDB; AAL51273.

PT Use of anti-idiotypic antibodies for human milk fat globules (HMG) - or
PT carcinoembryonic antigen (CEA)-associated tumor for delaying the
PT development of, or treating a HMG- or CEA-associated tumor (e.g. breast
PT tumor) in humans.
XX

Claim 2; Fig 1; 98pp; English.

CC The invention comprises a method for delaying the development of, or
CC treating a tumor that is associated with human milk fat globules (HMG)
CC or carcinoembryonic antigen (CEA). The method of the invention involves
CC administering an anti-idiotypic antibody for HMG (e.g. 11D10), and an
CC anti-idiotypic antibody for CEA (e.g. 3H1). The method is useful for
CC delaying the development, of or treating HMG/CEA-associated tumours. The
CC present amino acid sequence represents the light chain variable region of
CC the mouse 11D10 anti-idiotypic antibody
XX
SQ Sequence 145 AA;

Query Match 100.0%; Score 740; DB 6; Length 145;
Best Local Similarity 100.0%; Pred. No. 3e-48;
Matches 145; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGAPAIIGFLLLPFGTRCDIQMTQSPSSLSASLGQRVSLTCRASODIGINLHMLQOEP 60
DB 1 MGAPAIIGFLLLPFGTRCDIQMTQSPSSLSASLGQRVSLTCRASODIGINLHMLQOEP 60
QY 61 DGTIKRLIYATSSLSGSGVPKRFSGSGSDYSLTISLSIEDPFAVYCLQYASSPYTFGG 120
DB 61 DGTIKRLIYATSSLSGSGVPKRFSGSGSDYSLTISLSIEDPFAVYCLQYASSPYTFGG 120
QY 121 GTKLEIKRADAAPTVSIFFPSSKLG 145
DB 121 GTKLEIKRADAAPTVSIFFPSSKLG 145

RESULT 3
AAW87593
ID AAW87593 standard; protein; 145 AA.
XX
AC AAW87593;
XX
DT 16-MAR-1999 (first entry)
XX
DE Antibody 11D10 light chain variable region.
XX
XX Murine; mouse; antibody; light chain; variable region; anti-idiotypic;
KM human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT Protein /note="signal peptide"
FT 21..999
FT /note="mature protein"

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using bw model

Run on: December 6, 2004, 13:38:19 ; Search time 2233.74 Seconds
(without alignments)
7096.283 Million cell updates/sec

Title: US-08-836-455-1
Perfect score: 435
Sequence: 1 ATGGGGGGGGGGCTCTCAGAT.....CACCATCCAGTAGCTTGGG 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gse1.*
9: gb_gse2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	373.2	85.8	630	2	BF138788 601780387
2	362.8	83.4	926	4	BG962572 60282953
3	334	76.8	714	4	BG963548 60283126
4	320.2	73.6	374	5	BY083003
5	287.8	66.2	827	4	BI152061 602916512
6	287.6	66.1	874	4	BG518527 602578261
7	286.8	65.9	891	2	BF579432 602093833
8	285.2	65.6	626	2	BF582283 602101109
9	285.2	65.6	725	2	BF580940 602100636
10	282.8	65.0	1459	5	BQ918407 AGENCOURT
11	278.8	64.1	762	2	BF144806 601791486
12	278	63.9	901	5	BQ943305 AGENCOURT
13	276.4	63.5	772	2	BF581992 602099448
14	276.4	63.5	830	4	BI455041 603173343
15	275.6	63.4	695	2	BE284224 601099161
16	274.8	63.2	669	2	BF123422 601760623
17	274.8	62.8	708	4	BI103114 602889345
18	273.2	62.8	886	4	BG756818 602710291
19	269.2	61.9	658	6	CF108834 Shultzoni
20	268.8	61.8	685	4	BG518543 602578277
21	266.8	61.3	617	6	CD689887 EST6410 h
22	266.8	61.3	697	6	CD698986 EST16420
23	266.8	61.3	698	6	CD691710 EST8233 h
24	266.8	61.3	952	7	COS79354 ILLUMINIGEN

25	266.8	61.3	969	5	BU899279
26	265.2	61.0	464	5	BX480430
27	265.2	61.0	547	6	CD704894
28	265.2	61.0	764	6	CB956251
29	265.2	61.0	1019	4	BM914405
30	264.4	60.8	354	5	BY085718
31	263.6	60.6	545	6	CD697196
32	263.6	60.6	550	6	CD709576
33	263.6	60.6	586	6	CD695617
34	263.6	60.6	658	6	CD701345
35	263.6	60.6	723	6	CB956143
36	263.6	60.6	992	2	BF976253
37	262.8	60.4	851	4	BI101548
38	262.8	60.4	1038	4	BG757218
39	262.2	60.3	966	2	BF578083
40	262	60.2	569	6	CD706691
41	262	60.2	616	6	CD684315
42	262	60.2	666	6	CD684691
43	262	60.2	837	6	CB984807
44	262	60.2	867	4	BG754732
45	262	60.2	939	5	BQ705876

ALIGNMENTS

RESULT 1
LOCUS BF138788 630 bp mRNA linear EST 24-OCT-2000
DEFINITION 601780387F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4008404 5',
mRNA sequence.
ACCESSION BF138788
VERSION BF138788.1 GI:10977828
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM9242 row: n column: 21
High quality sequence stop: 628.

FEATURES

source 1..630
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
/clone="IMAGE:4008404"
/tissue_type="tumour, metastatic to mammary"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu30"
/note="Organ: lung; Vector: PCMV-SPORE6; Site 1: NotI;
Site 2: SalI; transgenic model MNT-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dT. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"

ORIGIN

Query Match 85.8%; Score 373.2; DB 2; Length 630;
Best local Similarity 92.3%; Pred. No. 2e-107;
Matches 393; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

QY	5	GGGCCCCCTGCTCAGATTCTTGGGTTCTGTGCTCTGTGTTCCAGGTAACCAAGATGTGACA	64
Db	1	GGGCTCTGTGGCGAGGTTTTTGGCTTCTGTGTGCTCTTGTTCAGGTGCCAGATGTGACA	60
QY	65	TCCAGATGACCACAGTCCATCTCTCTTATCTGCCTCTGTGGACAAAGAGTCAGTCTCA	124
Db	61	TCCAGATGACCACAGTCTCCATCTCTTATCTGCCTCTGTGGAGAAAGATCAGTCTCA	120
QY	125	CTTGTGGGGGAAGTCAAGACATTGGTATTAATTACATTATGGCTTCAAGAGAACGAGATG	184
Db	121	CTTGTGGGGGAAGTCAAGACATTGGTGTGGAGATTAACTGGTTTCAACAAGAAACGAGATG	180
QY	185	GAACTATTAAACGCTGATCTACAGCCACATCCAGTTTGGTTCTGTGTCCTCCAAAAGT	244
Db	181	GAACTATTAAAGCCCTGATCTACAGGCACATCCAGTTTGGATTCTGTGTCCTCCAAAAGT	240
QY	245	TCAGTGGCAGTAGGTTGGGTCAGATTATTTCTTCACCATCAGACGCTTGAATCTGAAG	304
Db	241	TCAGTGGCAGTAGGTTGGGTCAGATTATTTCTTCACCATCAGACGCTTGAATCTGAAG	300
QY	305	AATTTGTAGCATTACTGCTACAAATATGCTAGTTCTCCGTAAACGTTTGGAGGGGGGA	364
Db	301	ACTTTGCAACATTTATCTGTATTACAAATATGCTAGTTATCTTCACGTTGGGTGGGGA	360
QY	365	CCAAGCTGGAATATAAAACGGGCTGATGCTGACCAACATGATATCCATTTCCACCAATCCA	424
Db	361	CCAAGCTGAGCTGAAAACGGGCTGATGCTGACCAACATGATATTTTCCACCAATCCA	420
QY	425	GTAAGC 430	
Db	421	GTGAGC 426	

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
BC962572	60282995371 NCI_CGAP_C024 Mus musculus CDNA clone IMAGE:4984788 5'	BC962572	GI:14350209	mus musculus (house mouse)	EST	mus musculus (house mouse)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 926)	NIH-MGC	http://mgc.nci.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
							Contact: Robert Strausberg, Ph.D.				
							Email: cgabds-romail.nih.gov				
							Tissue Procurement: Jeffrey E. Green, M.D.				
							CDNA Library Preparation: Life Technologies, Inc.				
							DNA Sequencing by: Incyte Genomics, Inc.				
							Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:				
							http://image.lnl.gov				
							plate: LLM10991 row: 1 column: 13				
							High quality sequence stop: 685.				
							Location/Qualifiers				
							1..926				

```

/lab_host="UDH10B (T1 phage-resistant)"
/clone_lib="NCI CGAP Co2a"
/notes="Organ: colon, Vector: pCMV-SPORT6, Site 1: NotI,
Site 2: SalI; Cloned unidirectionally. Primer: oligo dt
Average insert size 1.6 kb. Constructed by life

```

Query Match	Best Local Similarity	83.4%;	Score 362.8;	DB 4;	Length 926;
Matches 188;	Conservative 0;	Mismatches 42;	Indels 0;	Gaps 0	
QY	1	ATGGGGGCCCCGCTCAGATTCCTTGGGTTCTTGTCCTTGGTTTCCAGGTACAGATGT	60		
Db	15	ATGAGGGTTCCCGTCACGTTTGGGCTTCTTGTCCTGTTCCAGGTACAGATGT	74		
QY	61	GACATCCAGATGACCCAGTCTTCATCTCTTATCTGCTCTTGGGCAAAAGTCACT	120		
Db	75	GACATCCAGATGACCCAGTCTTCATCTCTTATCTGCTCTTGGGCAAAAGTCACT	134		
QY	121	CTCATCTTCCGGGCAAGTCAGGACATTTGGTATTACTTCAATTTGGCTTCACGAGAACCA	180		
Db	135	CTCATCTTCCGGGCAAGTCAGGAGTGTGTTCTTAACTTGGCTTCACCAAAAACCA	194		
QY	181	GATGAACTATTTAAACGCTGATCTACCCACATCCAGTTAGGTTCTGGTGTCCCAAA	240		
Db	195	GATGAACTTTTAAAGCGCTGATCTACGCCCAACACTTTAGTTCTGGTGTCCCAAA	254		
QY	241	AGCTTCAGTGGCAGTAGGTCTGGGTCAGATTATTTCTCACCATTCAGAGCTTGAAGTCT	300		
Db	255	AGGTTCAATGTGCACTAGGTCTGGGTCAGATTATTTCTCACCGTCAGTAGGCTTGAAGTCT	314		
QY	301	GAAGATTTTGTAGGCTATTACTGTCTCAATATGCTAGTTCTCCGTACAGCTTGGAGGG	360		
Db	315	GAAGATTTTGTAGGCTATTTACTGTCTCAATATGCTAATTAATCCGTGAGCTTGGTGA	374		
QY	361	GGGACCAAGCTGGAATTAACCGGCTGATGCTGCACCAACTGATCATCTTCCACCA	420		
Db	375	GGGACCAAGGCTGGAATTAACCGGCTGATGCTGCACCAACTGATCATCTTCCACCA	434		
QY	421	TCCAGTAGC	430		
Db	435	TCCAGTAGC	444		

[illegible]

```
FEATURES
    source      location/Qualifiers
1. 714
    /organism="Mus musculus"
    /mol_type="mRNA"
    /strain="FVB/N"
    /db_xref="taxon:10090"
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 13:38:54 ; Search time 63.1138 Seconds
(without alignments)
4898.976 Million cell updates/sec

Title: US-08-836-455-1

Perfect score: 435
Sequence: 1 ATGGGGGGCCCTGCTCAGAT.....CACCATCCAGTACGTTGGG 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA:*
1: /cgn2_6/prodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/prodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/prodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/prodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/prodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/prodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB	ID	Description
1	435	100.0	435	3	US-09-096-244-1	Sequence 1, Appl1
2	323.4	74.3	387	3	US-08-943-136-1	Sequence 1, Appl1
3	323.4	74.3	387	3	US-08-973-518-1	Sequence 1, Appl1
4	309.4	71.1	732	2	US-08-356-786-3	Sequence 3, Appl1
5	309.4	71.1	739	1	US-08-133-804-5	Sequence 5, Appl1
6	309.4	71.1	739	1	US-08-461-838-5	Sequence 5, Appl1
7	309.4	71.1	739	2	US-08-461-838-5	Sequence 5, Appl1
8	305.2	70.2	1605	2	US-08-356-786-9	Sequence 9, Appl1
9	300.2	69.0	321	3	US-08-483-749A-25	Sequence 25, Appl1
10	292.2	67.2	321	2	US-08-888-366-13	Sequence 13, Appl1
11	292.2	67.2	321	2	US-08-888-366-19	Sequence 19, Appl1
12	291.2	66.9	321	2	US-08-888-366-25	Sequence 25, Appl1
13	284.4	65.4	456	4	US-09-318-786-26	Sequence 26, Appl1
14	282.4	64.9	867	4	US-09-318-786-38	Sequence 38, Appl1
15	267.6	61.5	447	2	US-08-579-940-1	Sequence 1, Appl1
16	267.6	61.5	447	2	US-08-838-692-3	Sequence 3, Appl1
17	266.6	61.3	321	3	US-08-483-749A-27	Sequence 27, Appl1
18	265.2	61.0	449	1	US-08-480-434-61	Sequence 61, Appl1
19	263.6	61.0	449	4	US-08-053-451B-61	Sequence 61, Appl1
20	263.6	60.6	714	4	US-09-472-087-62	Sequence 62, Appl1
21	263.2	60.5	276	3	US-08-373-146-52	Sequence 52, Appl1
22	262	60.2	439	3	US-09-042-353-360	Sequence 360, App
23	262	60.2	439	3	US-08-758-417A-208	Sequence 208, App
24	261.6	60.1	276	2	US-08-273-146-44	Sequence 44, Appl1
25	260.4	59.9	1066	2	US-08-157-101A-4	Sequence 4, Appl1
26	258.8	59.5	751	5	PCT-US94-07659-3	Sequence 3, Appl1
27	258.8	59.5	3819	3	US-09-042-353-393	Sequence 393, App

28	258.8	59.5	3819	3	US-08-758-417A-243	Sequence 243, App
29	258.8	59.5	19040	4	US-09-343-485A-3	Sequence 3, Appl1
30	258.6	59.4	393	1	US-08-236-520-1	Sequence 1, Appl1
31	258.6	59.4	393	5	PCT-US95-05262-1	Sequence 1, Appl1
32	252	57.9	381	1	US-08-137-117D-28	Sequence 28, Appl1
33	252	57.9	381	1	US-08-436-717-28	Sequence 28, Appl1
34	250.6	57.6	321	3	US-08-871-488A-16	Sequence 16, Appl1
35	248.4	57.1	642	2	US-08-634-783A-2	Sequence 2, Appl1
36	248.4	57.1	642	3	US-09-070-817-2	Sequence 2, Appl1
37	248	57.0	408	1	US-08-408-133-5	Sequence 5, Appl1
38	248	57.0	408	1	US-08-454-683-5	Sequence 5, Appl1
39	248	57.0	408	2	US-08-454-680-5	Sequence 5, Appl1
40	248	57.0	408	4	US-09-225-322B-9	Sequence 9, Appl1
41	248	57.0	408	4	US-09-764-304-9	Sequence 9, Appl1
42	247.6	56.9	705	1	US-08-488-376-16	Sequence 16, Appl1
43	247.6	56.9	705	2	US-08-634-223-16	Sequence 16, Appl1
44	247.6	56.9	705	2	US-08-634-224-16	Sequence 16, Appl1
45	247.6	56.9	705	2	US-08-634-400-16	Sequence 16, Appl1

ALIGNMENTS

RESULT 1
US-09-096-244-1
; Sequence 1, Application US/09096244
; Patent No. 6274143
; GENERAL INFORMATION:
; APPLICANT: Chatterjee, Malaya
; TITLE OF INVENTION: METHODS OF DELAYING DEVELOPMENT OF
; TITLE OF INVENTION: HMGs-ASSOCIATED TUMORS USING ANTI-IDIOTYPE ANTIBODY 11D10
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FORSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/096,244
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Polizzzi, Catherine M.
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 30414-20006.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 435 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..435
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 61
; US-09-096-244-1
Query Match 100.0%; Score 435; DB 3; Length 435;

Best Local Similarity 100.0%; Pred. No. 7.8e-132;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGGGGCCCCCTGCTCAGATTCTTGGGTTCTTGTGCTGTTTCCAGGTACCAATGT 60
DB 1 ATGGGGCCCCCTGCTCAGATTCTTGGGTTCTTGTGCTGTTTCCAGGTACCAATGT 60
QY 61 GACATCCAGATGACCCAGTCTCCATCCTCTTANCTGCGCTCTGGGACAAAGATCAGT 120
DB 61 GACATCCAGATGACCCAGTCTCCATCCTCTTANCTGCGCTCTGGGACAAAGATCAGT 120
QY 121 CTCACCTTGTGCGGCAAGTCAGACATGTGATTAATTAATTAATTAATTAATTAATTA 180
DB 121 CTCACCTTGTGCGGCAAGTCAGACATGTGATTAATTAATTAATTAATTAATTAATTA 180
QY 181 GATGGAACATTAATTAAGCCCTGATCTACGCCATCCAGTTCAGTTAGGTTCTGTCCTCCAAA 240
DB 181 GATGGAACATTAATTAAGCCCTGATCTACGCCATCCAGTTCAGTTAGGTTCTGTCCTCCAAA 240
QY 241 AGGTCAGTGGCAGTAGTCTGGGTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
DB 241 AGGTCAGTGGCAGTAGTCTGGGTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
QY 301 GAAATTTTGTAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
DB 301 GAAATTTTGTAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
QY 361 GGGACCAAGCTGGAATTAAGCGGCTGATGCTGACCAACGATGATCCATTTCCACCA 420
DB 361 GGGACCAAGCTGGAATTAAGCGGCTGATGCTGACCAACGATGATCCATTTCCACCA 420
QY 421 TCCAGTAAGCTGGG 435
DB 421 TCCAGTAAGCTGGG 435
```

RESULT 2

US-08-943-136-1
Sequence 1, Application US/08943136
Patent No. 6291208
GENERAL INFORMATION:
APPLICANT: Anand, Naveen N
APPLICANT: Barber, Brian H
APPLICANT: Cates, George A
APPLICANT: Caterini, Judith E
APPLICANT: Klein, Michel H
TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943.136
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/483,576
FILING DATE: 07-JUNE-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-733

TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-943-136-1

Query Match 74.3%; Score 323.4; DB 3; Length 387;
Best Local Similarity 90.6%; Pred. No. 1.5e-95;
Matches 345; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

```
QY 1 ATGGGGCCCCCTGCTCAGATTCTTGGGTTCTTGTGCTGTTTCCAGGTACCAATGT 60
DB 7 ATGAGGGTTCTGCTCAGATTCTTGGGTTCTTGTGCTGTTTCCAGGTACCAATGT 66
QY 61 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCTCTGCGACAAAGATCAGT 120
DB 67 GACATCCAGATGACCCAGTCTCCATCCTCTTATCTGCTCTGCGACAAAGATCAGT 126
QY 121 CTCACCTTGTGCGGCAAGTCAGACATGTGATTAATTAATTAATTAATTAATTAATTA 180
DB 127 CTCACCTTGTGCGGCAAGTCAGACATGTGATTAATTAATTAATTAATTAATTAATTA 186
QY 181 GATGGAACATTAATTAAGCCCTGATCTACGCCATCCAGTTCAGTTAGGTTCTGTCCTCCAAA 240
DB 187 GATGGAACATTAATTAAGCCCTGATCTACGCCATCCAGTTCAGTTAGGTTCTGTCCTCCAAA 246
QY 241 AGGTCAGTGGCAGTAGTCTGGGTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 300
DB 247 AGGTCAGTGGCAGTAGTCTGGGTGATTAATTAATTAATTAATTAATTAATTAATTAATTA 306
QY 301 GAAATTTTGTAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 360
DB 307 GAAATTTTGTAGCTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 366
QY 361 GGGACCAAGCTGGAATTAAGCGGCTGATGCTGACCAACGATGATCCATTTCCACCA 387
DB 367 GGGACCAAGCTGGAATTAAGCGGCTGATGCTGACCAACGATGATCCATTTCCACCA 387
```

RESULT 3

US-08-973-518-1
Sequence 1, Application US/08973518
Patent No. 6328962
GENERAL INFORMATION:
APPLICANT: Anand, Naveen N
APPLICANT: Barber, Brian H
APPLICANT: Cates, George A
APPLICANT: Caterini, Judith E
APPLICANT: Klein, Michel H
TITLE OF INVENTION: CHIMERIC ANTIBODIES FOR DELIVERY OF
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,518
FILING DATE: 07-APR-1998
CLASSIFICATION: 424

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 13:36:24 ; Search time 333.047 Seconds
(without alignments)
6856.387 Million cell updates/sec

Title: US-08-836-455-1
Perfect score: 435
Sequence: 1 ATGGGGGCCCCCTGCTCAGAT.....CACCATCCAGTAAGCTTGGG 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	100.0	435	2	AAT85149
2	435	100.0	435	2	AAV83772
3	435	100.0	435	8	AAI51273
4	394.8	90.8	450	1	AAH30165
5	384.6	88.4	407	3	AAZ49548
6	382.2	87.9	842	12	ADK67935
7	372.4	85.6	435	12	ADU57087
8	372.4	85.5	402	12	ADJ26724
9	329.6	75.8	390	9	AAI57230
10	324.2	74.5	351	12	ADJ26735
11	323.4	74.3	387	2	AAV77851
12	323.4	74.3	387	6	AAH31138
13	323.4	74.3	387	12	ADJ31872
14	323.4	74.3	351	12	ADJ26652
15	311.2	71.5	324	12	ADJ26703
16	309.4	71.1	729	2	AAQ46084
17	309.4	71.1	729	2	AAI36880
18	309.4	71.1	729	2	AAV21798
19	309.4	71.1	729	2	AAV63399
20	309.4	71.1	729	10	AAH61485
21	308.6	70.9	324	8	ADA45518

22	308.4	70.9	729	3	AAZ49543	AAZ49543 pBacFv#12
23	307.4	70.7	711	3	AAZ49542	AAZ49542 pBacFv#12
24	306.4	70.4	324	3	AAZ49534	AAZ49534 Mouse ant
25	302	69.4	1605	2	AAQ46086	AAQ46086 Sequence
26	301.4	69.3	756	6	AAH97136	AAH97136 P4-3 sing
27	301.4	69.3	771	6	AAH97142	AAH97142 P5-10 sing
28	301.4	69.3	1497	6	AAH97145	AAH97145 3B10XP4-3
29	300.2	69.0	321	3	AAH38908	AAH38908 520C9 hyb
30	292.2	67.2	321	2	AAQ97504	AAQ97504 Light cha
31	292.2	67.2	321	2	AAQ97507	AAQ97507 Light cha
32	292	67.1	324	12	ADQ60441	ADQ60441 Mouse ant
33	291.2	66.9	321	2	AAQ97510	AAQ97510 Light cha
34	284.4	65.4	432	2	AAQ15114	AAQ15114 IL-2 chim
35	284.4	65.4	456	4	AAQ66996	AAQ66996 Filamento
36	282.8	65.0	432	2	AAQ15113	AAQ15113 IL-2 chim
37	282.4	64.9	867	4	AAQ67002	AAQ67002 Filamento
38	273	62.8	297	12	ADM78076	ADM78076 Human SJA
39	270	62.1	981	12	ADP07904	ADP07904 Human Imm
40	269.2	61.9	642	12	ADN41869	ADN41869 Nucleotid
41	268.4	61.7	438	4	AAH41157	AAH41157 Human cod
42	268.4	61.7	463	8	AAH56221	AAH56221 Human AB-
43	268.4	61.7	6082	8	AAH56212	AAH56212 Human AB-
44	267.6	61.5	447	2	AAH31540	AAH31540 3H1 Light
45	267.6	61.5	447	2	AAH34541	AAH34541 Monoclonal

ALIGNMENTS

RESULT 1	AAH85149	AAH85149 standard; cDNA; 435 BP.
ID	AAH85149	
AC	AAH85149	
XX	25-MAR-2003 (revised)	
DT	04-JUN-1998 (first entry)	
XX	Murine monoclonal anti-idiotypic antibody 11D10 VL cDNA.	
XX	Monoclonal anti-idiotypic antibody 11D10; mucin;	
KW	human milk fat globule; HMFG; tumour; breast cancer; vaccine; ss.	
XX	Mus musculus.	
OS	Key	Location/Qualifiers
XX	sig_peptide	1..60
FT	mat_peptide	/*tag= a
FT		61..435
FT		/*tag= b
XX	WO9722699-A2.	
PN	26-JUN-1997.	
XX	19-DEC-1996;	96MO-US020757.
XX	20-DEC-1995;	95US-00575762.
PR	26-JAN-1996;	96US-00591655.
PR	13-DEC-1996;	96US-00766350.
XX	(KENT) UNIV KENTUCKY.	
XX	Chatterjee M, Foon KA, Chatterjee SK,	
PI	WPI; 1997-341690/31.	
DR	P-PDB; AAW27119.	
XX	Monoclonal anti-idiotypic antibody 11D10 - elicits immune response against	
PT	human milk fat globule disease associated tumours, especially breast	
XX	cancer.	
PS	Claim 11; Page 94; 130pp; English.	

XX This cDNA sequence encodes the light chain variable region VL (AA085149)
CC of monoclonal anti-idiotypic antibody 11D10 produced by hybridoma cell
CC line ATCC 12020. 11D10 was obtained by immunising naive mice with MC-10
CC anti-HMG antibody to obtain an anti-idiotypic response. It elicits an
CC immune response against a specific epitope of a high mol.wt. mucin of
CC human milk fat globule (HMG). It induces an immunological response to
CC HMG in mice, rabbits, monkeys and patients with advanced HMG-associated
CC tumours. Pharmacological compositions and vaccines comprising 11D10, 11D10
CC polypeptides and/or 11D10 polynucleotides are claimed. Also claimed are
CC diagnostic kits and methods of using 11D10, 11D10 polypeptides and/or
CC 11D10 polynucleotides, including methods of treating HMG-associated
CC tumours. (Updated on 25-MAR-2003 to correct PR field.)
XX

SO Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 U; 0 Other;

Query Match 100.0%; Score 435; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 5.6e-127;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGCCCCCTGCTGAGATTCCTGGGCTCTGTTGCTCTGTTCCAGGTACAGATGT 60
DB 1 ATGGGGGCCCCCTGCTGAGATTCCTGGGCTCTGTTGCTCTGTTCCAGGTACAGATGT 60
QY 61 GACATCCAGATGACCCAGTCTCCATCTCTTAATGCTCTCTGGGACAAAGATCAGT 120
DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTAATGCTCTCTGGGACAAAGATCAGT 120
QY 121 CTGACTTGTGGGCAAGTCCAGATCTGATTTAATCTTACATTTGCTTCAGAGAACCA 180
DB 121 CTGACTTGTGGGCAAGTCCAGATCTGATTTAATCTTACATTTGCTTCAGAGAACCA 180
QY 181 GATGGAATCTTAAAGCCGTGATCTACGACCATCCAGTTAGTCTGGTCCCCCA 240
DB 181 GATGGAATCTTAAAGCCGTGATCTACGACCATCCAGTTAGTCTGGTCCCCCA 240
QY 241 AGGTTGAGTGGCGATGAGTGTGGGTCAATTAATCTTCAACATCCAGACCTTGAAGTCT 300
DB 241 AGGTTGAGTGGCGATGAGTGTGGGTCAATTAATCTTCAACATCCAGACCTTGAAGTCT 300
QY 301 GAAGATTTGTGATGCTTATTAATCTGCTCAATTAATGCTTCCGATCAGCTTGGAGGG 360
DB 301 GAAGATTTGTGATGCTTATTAATCTGCTCAATTAATGCTTCCGATCAGCTTGGAGGG 360
QY 361 GGGACCAAGCTGGAATAAAGCGGCTGATGCTGACCAATGATTCATCTTCCACCA 420
DB 361 GGGACCAAGCTGGAATAAAGCGGCTGATGCTGACCAATGATTCATCTTCCACCA 420
QY 421 TCCAGTAAGCTTGGG 435
DB 421 TCCAGTAAGCTTGGG 435

RESULT 2
AA083772
ID AA083772 standard; cDNA; 435 BP.

XX AA083772;

XX 16-MAR-1999 (first entry)

XX Antibody 11D10 light chain variable region coding sequence.

XX Murine; mouse; antibody; light chain; variable region; anti-idiotypic; ss;
XX human milk fat globule; tumour; ovary; lung; pancreas; carcinoma; breast.
OS Mus sp.

XX Key Location/Qualifiers

FT CDS 1..435
FT /tag= a
FT /product= "antibody 11D10 light chain variable region"
FT /transl_except= (pos:163..165, aa:Thr)

FT /note= "no stop codon is given at the 3' end of the
FT sequence"
FT sig_peptide 1..60
FT /tag= b
FT mat_peptide 61..435
FT /tag= c

XX W09856419-A1.

XX 17-DEC-1998.

XX 12-JUN-1998; 98WO-US012250.

XX 13-JUN-1997; 97US-0049540P.

XX 11-JUN-1998; 98US-00096244.

XX (KENT) UNIV KENTUCKY RES FOUND.

XX Chatterjee M, Foon KA;

XX WPI; 1999-060029/05.

XX P-PSDB; AA087593.

XX Delaying development of, or treating, HMG-associated tumours - using
XX anti-idiotypic antibody 11D10 raised against antibodies to human milk fat
XX globule protein.

XX Disclosure; Fig 1; 54pp; English.

XX This sequence represents the coding sequence for the murine antibody
XX 11D10 light chain variable region. This anti-idiotypic antibody is used to
XX delay the development of, or treat, a human milk fat globule (HMG)
XX associated tumour in an individual having low tumour burden. The antibody
XX 11D10 is used to prevent the recurrence of HMG-associated tumours e.g.
XX ovarian, non-small cell lung and pancreatic carcinoma, especially for
XX treating breast tumours

SO Sequence 435 BP; 100 A; 111 C; 102 G; 122 T; 0 U; 0 Other;

Query Match 100.0%; Score 435; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 5.6e-127;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGGGGCCCCCTGCTGAGATTCCTGGGCTCTGTTGCTCTGTTCCAGGTACAGATGT 60
DB 1 ATGGGGGCCCCCTGCTGAGATTCCTGGGCTCTGTTGCTCTGTTCCAGGTACAGATGT 60
QY 61 GACATCCAGATGACCCAGTCTCCATCTCTTAATGCTCTCTGGGACAAAGATCAGT 120
DB 61 GACATCCAGATGACCCAGTCTCCATCTCTTAATGCTCTCTGGGACAAAGATCAGT 120
QY 121 CTGACTTGTGGGCAAGTCCAGATCTGATTTAATCTTACATTTGCTTCAGAGAACCA 180
DB 121 CTGACTTGTGGGCAAGTCCAGATCTGATTTAATCTTACATTTGCTTCAGAGAACCA 180
QY 181 GATGGAATCTTAAAGCCGTGATCTACGACCATCCAGTTAGTCTGGTCCCCCA 240
DB 181 GATGGAATCTTAAAGCCGTGATCTACGACCATCCAGTTAGTCTGGTCCCCCA 240
QY 241 AGGTTGAGTGGCGATGAGTGTGGGTCAATTAATCTTCAACATCCAGACCTTGAAGTCT 300
DB 241 AGGTTGAGTGGCGATGAGTGTGGGTCAATTAATCTTCAACATCCAGACCTTGAAGTCT 300
QY 301 GAAGATTTGTGATGCTTATTAATCTGCTCAATTAATGCTTCCGATCAGCTTGGAGGG 360
DB 301 GAAGATTTGTGATGCTTATTAATCTGCTCAATTAATGCTTCCGATCAGCTTGGAGGG 360
QY 361 GGGACCAAGCTGGAATAAAGCGGCTGATGCTGACCAATGATTCATCTTCCACCA 420
DB 361 GGGACCAAGCTGGAATAAAGCGGCTGATGCTGACCAATGATTCATCTTCCACCA 420
QY 421 TCCAGTAAGCTTGGG 435
DB 421 TCCAGTAAGCTTGGG 435

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using bw model

Run on: December 6, 2004, 13:39:34 ; Search time 2290.55 Seconds
(without alignments)
8980.833 Million cell updates/sec

Title: US-08-836-455-1

Perfect score: 435
Sequence: 1 ATGGGGGCCCCCTGCTCAGAT.....CACCATCCAGTACGTTGGG 435

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

GenBank: 1: gb ba: *
2: gb ntg: *
3: gb_in: *
4: gb_cm: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pl: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	435	100.0	435	6	AR164505 Sequence
2	435	100.0	435	6	BD085737 Methods O
3	384.6	88.4	407	6	ES4981 Peptide. 1/
4	379.4	87.2	381	10	AF124721 Mus muscu
5	361.6	83.1	384	10	AB017434 Mus muscu
6	362.6	83.1	390	10	MUSIKCC L41880 Mus musculu
7	352.2	81.0	381	10	AF045508 Mus muscu
8	349.8	80.2	381	10	AF045495 Mus muscu
9	345.8	79.5	381	10	AF045510 Mus muscu
10	332	76.3	380	10	MMIGVJ1 X02177 M.musculu
11	327.2	75.2	381	10	MMIGVJ2 X02178 M.musculu
12	325.4	74.8	383	10	MUSIGKMA M12191 Mouse Ig ac
13	323.8	74.4	405	10	AB016620 Mus muscu
14	323.4	74.3	387	6	AR169918 Sequence
15	323.4	74.3	387	6	AR169918 Sequence
16	317.2	72.9	354	10	AB089681 Mus muscu
17	316	72.6	684	10	AB089681 Mus muscu
18	314.4	72.3	685	10	MMIGK7 V00808 Part of the
19	311.6	71.6	348	10	MMVJIG X54755 Mouse reatr

20	310.8	71.4	804	6	CQ768809	CQ768809 Sequence
21	310.8	71.4	804	6	CO802043	CO802043 Sequence
22	309.8	71.2	321	10	AR163749	AR163749 Mus muscu
23	309.4	71.1	739	6	AR007981	AR007981 Sequence
24	309.4	71.1	739	6	AR058996	AR058996 Sequence
25	309.4	71.1	739	6	123446	Sequence 5
26	308.6	70.9	324	6	AX722008	Sequence
27	308.4	70.9	729	6	ES4976	ES4976 Peptide. 1/
28	307.8	70.8	359	10	AY050275	AY050275 Mus muscu
29	307.6	70.7	324	10	MUSK	L48667 Mus musculu
30	307.4	70.7	711	6	ES4975	ES4975 Peptide. 1/
31	306.4	70.4	324	6	ES4967	ES4967 Peptide. 1/
32	305.4	70.2	328	10	MMU55591	U55591 Mus musculu
33	301.4	69.3	756	6	AX256284	AX256284 Sequence
34	301.4	69.3	771	6	AX256296	AX256296 Sequence
35	301.4	69.3	1497	6	AX256302	AX256302 Sequence
36	300.6	69.1	324	6	103643	103643 Sequence 4
37	300.6	69.1	324	6	107835	107835 Sequence 4
38	300.2	69.0	345	10	AY605279	AY605279 Mus muscu
39	299	68.7	323	10	AY229938	AY229938 Mus muscu
40	298.6	68.6	321	10	MUSIGKRA3	M59920 Mouse IG ge
41	298.4	68.6	348	10	AY245603	AY245603 Mus muscu
42	297.2	68.3	1019	10	BC027418	BC027418 Mus muscu
43	296.2	68.1	413	10	MUSIGKCLN	M20832 Mouse Igmk
44	295.6	68.0	972	10	AF466770	AF466770 Mus muscu
45	293.6	67.5	364	10	AY208321	AY208321 Mus muscu

ALIGNMENTS

RESULT 1	AR164505	Sequence 1 from patent US 6274143.	435 bp	DNA	linear	PAT 17-OCT-2001
LOCUS	AR164505	Sequence 1 from patent US 6274143.				
DEFINITION	AR164505	Sequence 1 from patent US 6274143.				
ACCESSION	AR164505	Sequence 1 from patent US 6274143.				
VERSION	AR164505.1	GI:16237555				
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 435)					
AUTHORS	Charterjee, M. and Poon, K. A.					
TITLE	Methods of delaying development of HMG-associated tumors using anti-idiotypic antibody 11D10					
JOURNAL	Patent: US 6274143-A 1 14-AUG-2001;					
FEATURES	Location/Qualifiers					
source	1..435					
ORIGIN	1..435					
Query Match	100.0%	Score 435;	DB 6;	Length 435;		
Best Local Similarity	100.0%	Pred. No. 1.9e-120;				
Matches	435;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	ATGGGGGCCCCCTGCTCAGATTTTGGGTTCTTGTCTCTTGTTCACGATACAGATGT	60			
DB	1	ATGGGGGCCCCCTGCTCAGATTTTGGGTTCTTGTCTCTTGTTCACGATACAGATGT	60			
QY	61	GACATCCAGATGACCCAGTCTCATCTCTTATTCGCGCTCTGGGACAAAGTCACT	120			
DB	61	GACATCCAGATGACCCAGTCTCATCTCTTATTCGCGCTCTGGGACAAAGTCACT	120			
QY	121	CTCACTTGTGGGCAAGTCAAGATTTGATTTAATTACATTTAGGCTTCAGACGAACCA	180			
DB	121	CTCACTTGTGGGCAAGTCAAGATTTGATTTAATTACATTTAGGCTTCAGACGAACCA	180			
QY	181	GATGAACCTATTAAAGCCTGATCTACGCCACATCCAGTTAGGTTGTGTGCCCAAA	240			
DB	181	GATGAACCTATTAAAGCCTGATCTACGCCACATCCAGTTAGGTTGTGTGCCCAAA	240			
QY	241	AGGTGAGTGGGAGTGGTGTGGGTGATTAATCTCAACCATCAGACGCTTAGGTCT	300			

Db 241 AGGTCAGTGGCAGTAGGTCTGGGTGAGATTATCTCTACCATCAGCAGCCTTGAGTCT 300
Qy 301 GAAGATTTTGTACCTTATTACTGTCTACAAATAGTACTTCTCCGACACGTTGGAGGG 360
Db 301 GAAGATTTTGTACCTTATTACTGTCTACAAATAGTACTTCTCCGACACGTTGGAGGG 360
Qy 361 GGGACCAAGCTGGAATTAACCGGGCTGATGTCGACCAACTGTATCCATCTCCGACCA 420
Db 361 GGGACCAAGCTGGAATTAACCGGGCTGATGTCGACCAACTGTATCCATCTCCGACCA 420
Qy 421 TCCAGTAAGCTTGGG 435
Db 421 TCCAGTAAGCTTGGG 435

RESULT 2
LOCUS BD085737 435 bp DNA linear PAT 27-AUG-2002
DEFINITION Methods of delaying development of HMGF-associated tumors using
anti-idiotypic antibody 11D10.
ACCESSION BD085737
VERSION BD085737.1 GI:22631347
KEYWORDS JP 2001523269-A/1.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 435)
AUTHORS Chatterjee M. and Foon K.A.
TITLE Methods of delaying development of HMGF-associated tumors using
anti-idiotypic antibody 11D10
JOURNAL Patent: JP 2001523269-A 1 20-NOV-2001;
THE UNIVERSITY OF KENTUCKY RESEARCH FOUNDATION
COMMENT OS JP 2001523269-A/1
PN JP 20-NOV-2001
PF 12-JUN-1998 JP 1999503252
PR 13-JUN-1997 US 60/049540,11-JUN-1998 US 09/096244 PI
MALAYA CHATTERJEE, KENNETH A FOON
PC A61K39/395,A61K39/39//C07K16/42
CC Strandedness: Single;
CC Topology: Linear;
CC Methods of delaying development of HMGF-associated tumors CC
using
CC anti-idiotypic antibody 11D10
FH Key Location/Qualifiers
FT CDS 1..435
FT mat_peptide 61..435
FT Location/Qualifiers
FEATURES
source 1..435
/organism="unclassified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN
Query Match 100.0%; Score 435; DB 6; Length 435;
Best Local Similarity 100.0%; Pred. No. 1,9e-120;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGGGCCCTGCTCAGATTCTTGGGTTCTTGTGCTTCTTTCACAGTACCGAGT 60
Db 1 ATGGGGGCCCTGCTCAGATTCTTGGGTTCTTGTGCTTCTTTCACAGTACCGAGT 60
Qy 61 GACATCCAGATGACCCAGTCTCCATCTCTATCTGCTCTGGGACAAAGATCAGT 120
Db 61 GACATCCAGATGACCCAGTCTCCATCTCTATCTGCTCTGGGACAAAGATCAGT 120
Qy 121 CTCACCTTGTGGGGCAAGTCAGACATTGGTATTAACTTACATTGGCTTCAGAGAACCA 180
Db 121 CTCACCTTGTGGGGCAAGTCAGACATTGGTATTAACTTACATTGGCTTCAGAGAACCA 180
Qy 181 GATGAACATATTAAACGCGCTGATCTACGCCACATCCATTAGTTCTGGTGTCCCAA 240

Db 181 GATGAACATATTAAACGCGCTGATCTACGCCACATCCATTAGTTCTGGTGTCCCAA 240
Qy 241 AGGTCAGTGGCAGTAGGTCTGGGTGAGATTATCTCTACCATCAGCAGCCTTGAGTCT 300
Db 241 AGGTCAGTGGCAGTAGGTCTGGGTGAGATTATCTCTACCATCAGCAGCCTTGAGTCT 300
Qy 301 GAAGATTTTGTACCTTATTACTGTCTACAAATAGTACTTCTCCGACACGTTGGAGGG 360
Db 301 GAAGATTTTGTACCTTATTACTGTCTACAAATAGTACTTCTCCGACACGTTGGAGGG 360
Qy 361 GGGACCAAGCTGGAATTAACCGGGCTGATGTCGACCAACTGTATCCATCTCCGACCA 420
Db 361 GGGACCAAGCTGGAATTAACCGGGCTGATGTCGACCAACTGTATCCATCTCCGACCA 420
Qy 421 TCCAGTAAGCTTGGG 435
Db 421 TCCAGTAAGCTTGGG 435

RESULT 3
LOCUS E54981 407 bp DNA linear PAT 31-JAN-2002
DEFINITION Peptide.
ACCESSION E54981
VERSION E54981.1 GI:18629719
KEYWORDS JP 2000236884-A/15.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 407)
AUTHORS Nishida, T., Okura, T., Tanimoto, T. and Kurimoto, M.
TITLE Peptide
JOURNAL Patent: JP 2000236884-A 15 05-SEP-2000;
HAYASHIBARA BIOCHEM LAB INC
COMMENT OS Mus musculus (mouse)
PN JP 2000236884-A/15
PD 05-SEP-2000
PF 24-JUN-1999 JP 1999177846
PR PI TAKEHIRO NISHIDA, TAKANORI OKURA, TADAO TANIMOTO, PI MASASHI
KURIMOTO
PC C12N15/09,A61K31/00,A61K39/395,A61K48/00,C07K16/24,C12P21/08,
C12N15/00
FH Key Location/Qualifiers
FT CDS (1)..(407)
FT sig_peptide (1)..(60).
FT Location/Qualifiers
FEATURES
source 1..407
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"

ORIGIN
Query Match 88.4%; Score 384.6; DB 6; Length 407;
Best Local Similarity 96.6%; Pred. No. 3.6e-105;
Matches 393; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 1 ATGGGGGCCCTGCTCAGATTCTTGGGTTCTTGTGCTTCTTTCACAGTACCGAGT 60
Db 1 ATGGGGGCCCTGCTCAGATTCTTGGGTTCTTGTGCTTCTTTCACAGTACCGAGT 60
Qy 61 GACATCCAGATGACCCAGTCTCCATCTCTATCTGCTCTGGGACAAAGATCAGT 120
Db 61 GACATCCAGATGACCCAGTCTCCATCTCTATCTGCTCTGGGACAAAGATCAGT 120
Qy 121 CTCACCTTGTGGGGCAAGTCAGACATTGGTATTAACTTACATTGGCTTCAGAGAACCA 180
Db 121 CTCACCTTGTGGGGCAAGTCAGACATTGGTATTAACTTACATTGGCTTCAGAGAACCA 180
Qy 181 GATGAACATATTAAACGCGCTGATCTACGCCACATCCATTAGTTCTGGTGTCCCAA 240